

#3

FIG. 1A

1 agggagagggc agtgaccatg aaggctgtgc tgcttgccct gttgatggca
51 ggcttgggccc tgcagccagg cactgccctg ctgtgctact cctgcaaagc
101 ccaggtgagc aacgaggact gcctgcaggt ggagaactgc acccagctgg
151 gggagcagtg ctggaccgcg cgcattccgcg cagttggcct cctgaccgtc
201 atcagcaaag gctgcagctt gaactgctg gatgactcac aggactacta
251 cgtgggcaag aagaacatca cgtgctgtga caccgacttg tgcaacgcca
301 gcggggccca tgccctgcag ccggtgccc ccattccttg gctgctccct
351 gcactcggcc tgctgctctg gggaccggc cagctatagg ctctgggggg
401 ccccgctgca gccacactg ggtgtggtgc cccaggcctt tgtgccactc
451 ctcacagaac ctggcccagt gggagcctgt cctgggttcct gaggcacatc
501 ctaacgcaag tttgaccatg tatgtttgca ccccttttcc ccnaaccctg
551 accttcccat gggccttttc caggattccn accnggcaga tcagttttag
601 tganacanat ccgcntgcag atggccctc caaccnttn tgttgntggt
651 tccatggccc agcattttcc acccttaacc ctgtgttcag gcacttnttc
701 ccccaggaag ccttccctgc ccacccatt tatgaattga gccaggtttg
751 gtccgtggtg tccccgcac ccagcagggg acaggcaatc aggagggccc
801 agtaaaggct gagatgaagt ggactgagta gaactggagg acaagagttg
851 acgtgagttc ctgggagttt ccagagatgg ggcctggagg cctggaggaa
901 ggggccaggc ctcacatttg tgggntccc gaatggcagc ctgagcacag
951 cgtaggccct taataaacac ctgttgata agccaaaaaa aaaaaaa

FIG. 1B

MKAVLLALLMAGLALQPGTALLCYSCKAQVSNEDECLQV
ENCTQLGEQCWTARIRAVGLLTVISKGCSLNCVDDS
QDYVVGKKNITCCDTLDCNASGAHALQPAAAILALLPAL
GLLLWGPGQL

FIG. 2

1 ATGAAGACAGTTTTTTTTATCCTGCTGGCCACCTACTTAGCCCTGCATCCAGGTGCTGCT
 -----+-----+-----+-----+-----+-----+ 60
 TACTTCTGTCAAAAAAATAGGACGACCGGTGGATGAATCGGGACGTAGGTCCACGACGA

 M K T V F F I L L A T Y L A L H P G A A

 61 CTGCAGTGCTATTCATGCACAGCACAGATGAACAACAGAGACTGTCTGAATGTACAGAAC
 -----+-----+-----+-----+-----+-----+ 120
 GACGTACAGATAAGTACGTGTCGTGTCTACTTGTGTCTCTGACAGACTTACATGTCTTG

 L Q C Y S C T A Q M N N R D C L N V Q N

 121 TGCAGCCTGGACCAGCACAGTTGCTTTACATCGCGCATCCGGGCCATTGGACTCGTGACA
 -----+-----+-----+-----+-----+-----+ 180
 ACGTCGGACCTGGTCGTGTCAACGAAATGTAGCGCGTAGGCCCGGTAACCTGAGCACTGT

 C S L D Q H S C F T S R I R A I G L V T

 181 GTTATCAGTAAGGGCTGCAGCTCACAGTGTGAGGATGACTCGGAGAACTACTATTTGGGC
 -----+-----+-----+-----+-----+-----+ 240
 CAATAGTCATTCCCAGCTCGAGTGTCACTCCTACTGAGCCTCTTGATGATAAACCCG

 V I S K G C S S Q C E D D S E N Y Y L G

 241 AAGAAGAACATCACGTGCTGCTACTCTGACCTGTGCAATGTCAACGGGGCCACACCCTG
 -----+-----+-----+-----+-----+-----+ 300
 TTCTTCTGTAGTGACGACGATGAGACTGGACACGTTACAGTTGCCCGGGTGTGGGAC

 K K N I T C C Y S D L C N V N G A H T L

 301 AAGCCACCCACCCCTGGGGCTGCTGACCGTGTCTGACGCTGTTGCTGTGGGGCTCC
 -----+-----+-----+-----+-----+-----+ 360
 TTCGGTGGGTGGTGGGACCCGACGACTGGCACGAGACGTCGGACAACGACACCCCGAGG

 K P P T T L G L L T V L C S L L L W G S

 361 AGCCGTCTGTAGGCTCTGGGAGAGCCTACCATAGCCCGATTGTGAAGGGATGAGCTGCAC
 -----+-----+-----+-----+-----+-----+ 420
 TCGGCAGACATCCGAGACCCTCTCGGATGGTATCGGGCTAACACTTCCCTACTCGACGTG

 S R L *

 421 TCCACCCACCCCCACACAGG
 -----+-----+ 441
 AGGTGGGGTGGGGTGTGTCC

495249 63433823

FIG. 3

1	M	K	I	F	L	P	V	L	L	A	A	L	L	G	V	E	R	A	S	S	hSCA-2
1	M	K	A	V	L	L	A	L	L	M	A	G	L	A	L	Q	P	G	T	A	hPSCA
1	M	K	T	V	L	F	L	L	A	T	Y	L	A	L	H	P	G	A	A	mPSCA	
21	L	M	C	F	S	C	L	N	Q	K	S	N*	L	Y	C	L	K	P	T	I	
21	L	L	C	Y	S	C	K	A	Q	V	S	N*	E	D	C	L	Q	V	E	N*	
21	L	Q	C	Y	S	C	T	A	Q	M	N	N*	R	D	C	L	N	V	Q	N*	
41	C	S	D	Q	D	N	Y	C	V	T	V	S	A	S	A	G	I	G	N	L	
41	C	T	Q	L	G	E	Q	C	W	T	A	R	I	R	A	V	G	L	L	T	
41	C	S	L	D	Q	H	S	C	F	T	S	R	I	R	A	I	G	L	V	T	
61	V	T	F	G	H	S	L	S	K	T	C	S	P	A	C	P	I	P	E	G	
61	V	-	-	-	-	-	I	S	K	G	C	S	L	N	C	V	D	D	S	Q	
61	V	-	-	-	-	-	I	S	K	G	C	S	S	Q	C	E	D	D	S	E	
81	V	N	V	G	V	A	S	M	G	I	S	C	C	Q	S	F	L	C	N*	F	
76	D	Y	Y	V	G	K	K	-	N*	I	T	C	C	D	T	D	L	C	N*	A	
76	N	Y	Y	L	G	K	K	-	N*	I	T	C	C	Y	S	D	L	C	N*	V	
101	S	A	A	D	G	G	L	R	A	S	V	T	L	L	G	A	G	L	L	L	
95	S	G	A	H	A	L	Q	P	A	A	A	I	L	A	L	L	P	A	L	G	
95	N	G	A	H	T	L	K	P	P	T	T	L	G	L	L	T	V	L	C	S	
121	S	L	L	P	A	L	L	R	F	G	P										
115	L	L	L	W	G	P	G	Q	L	-	-										
115	L	L	L	W	G	S	S	R	L	-	-										

0085453.073604

FIG. 4

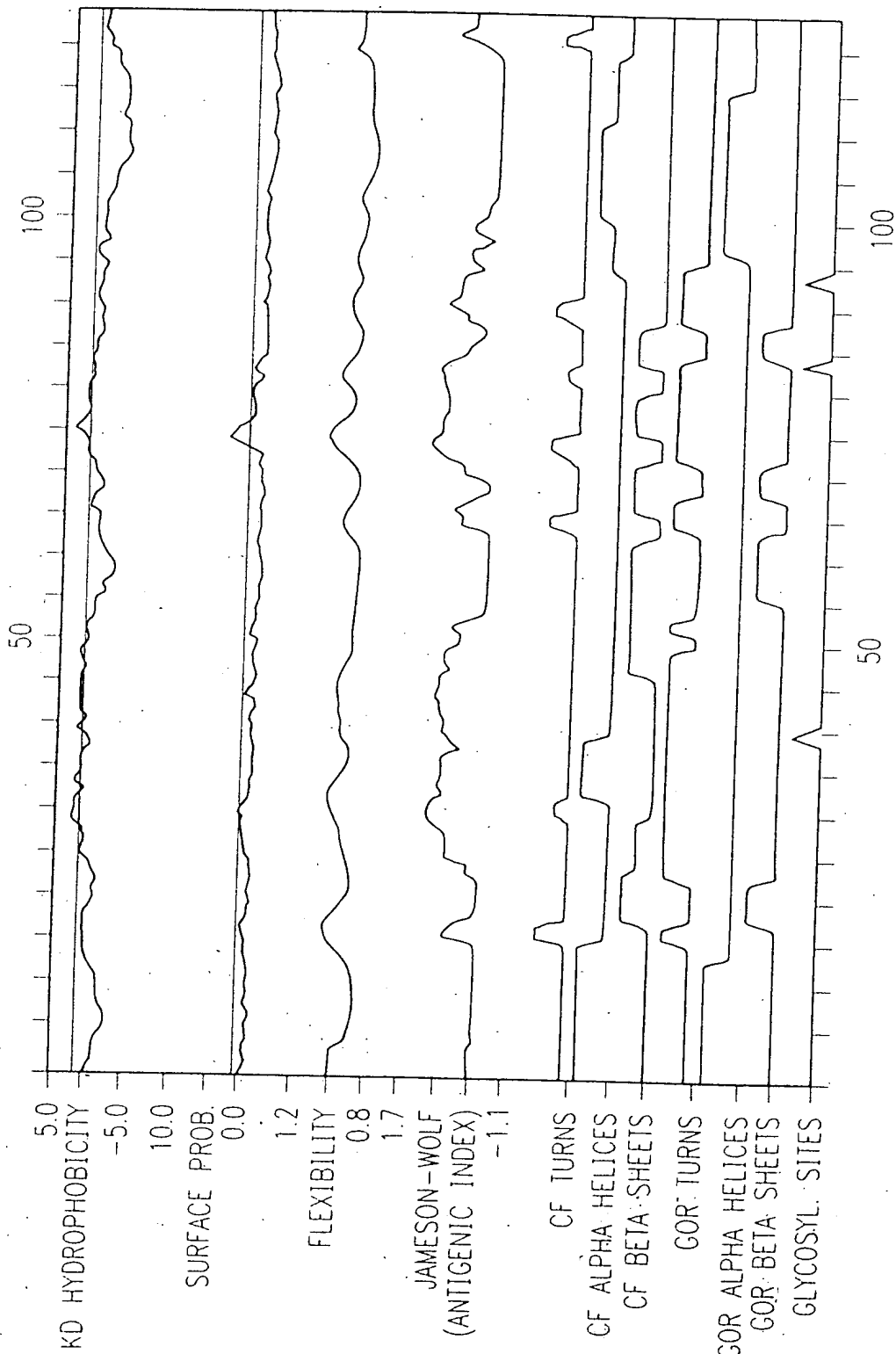
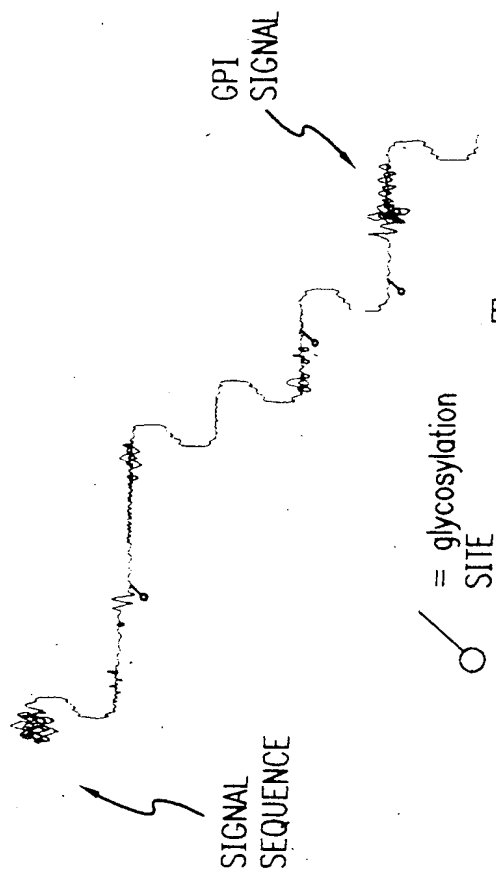


FIG. 5



LAPC9
S. INTESTINE
TESTIS
KIDNEY
KIDNEY
BLADDER CARCINOMA
BLADDER
BLADDER
PROSTATE
PROSTATE
PROSTATE

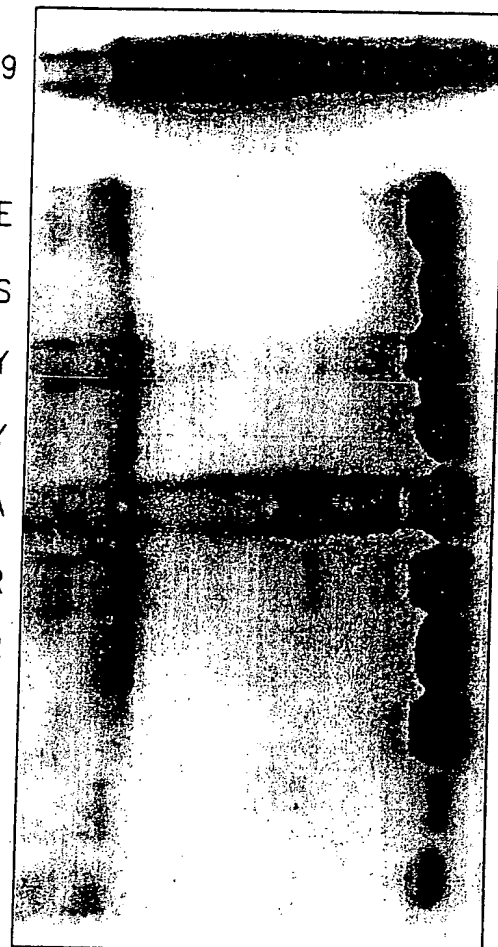


FIG. 6

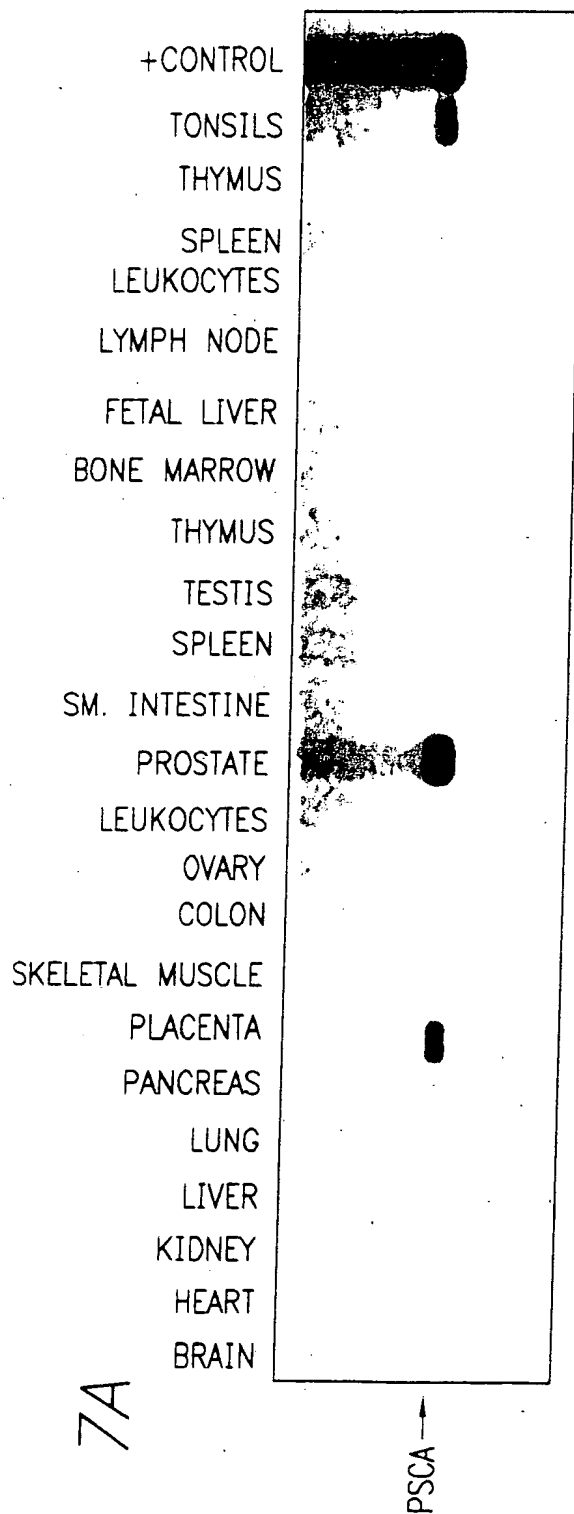


FIG. 7A

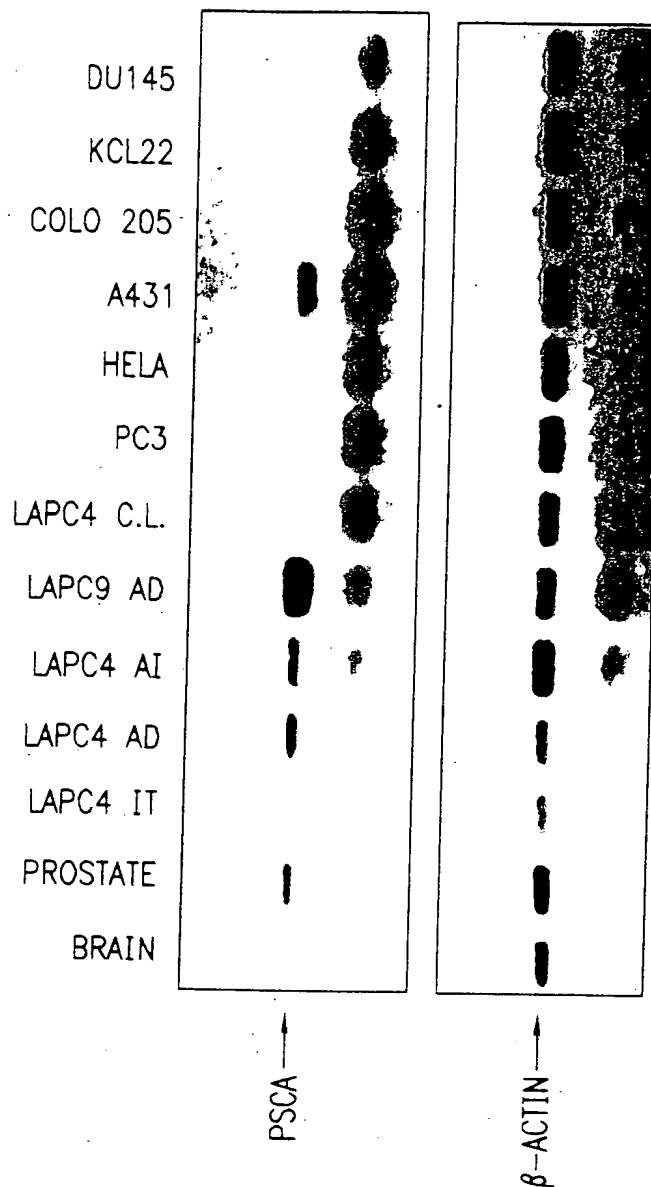


FIG. 7B

FIG. 8A

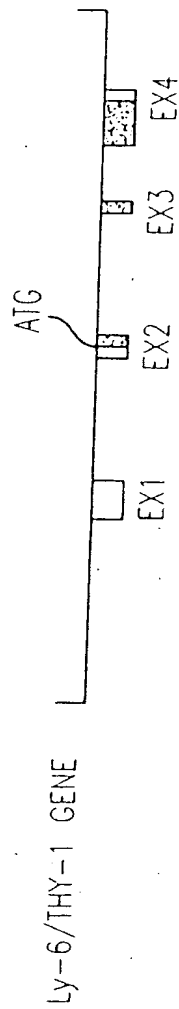


FIG. 8B

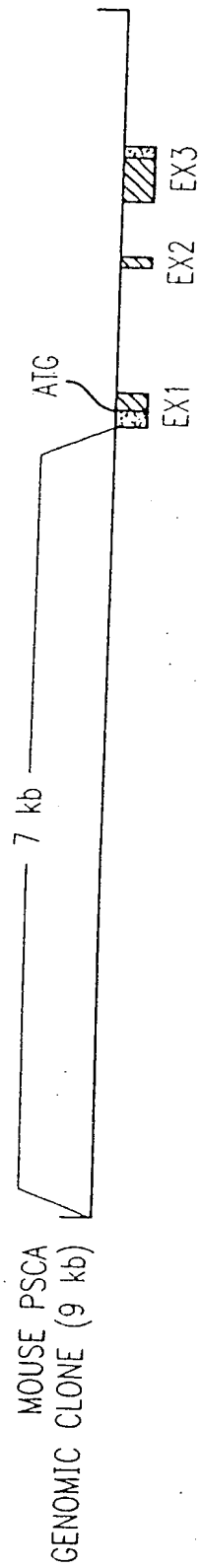
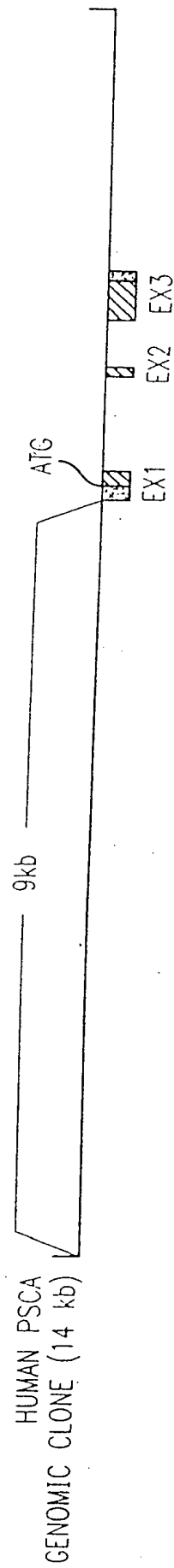


FIG. 8C



405220" 69459000

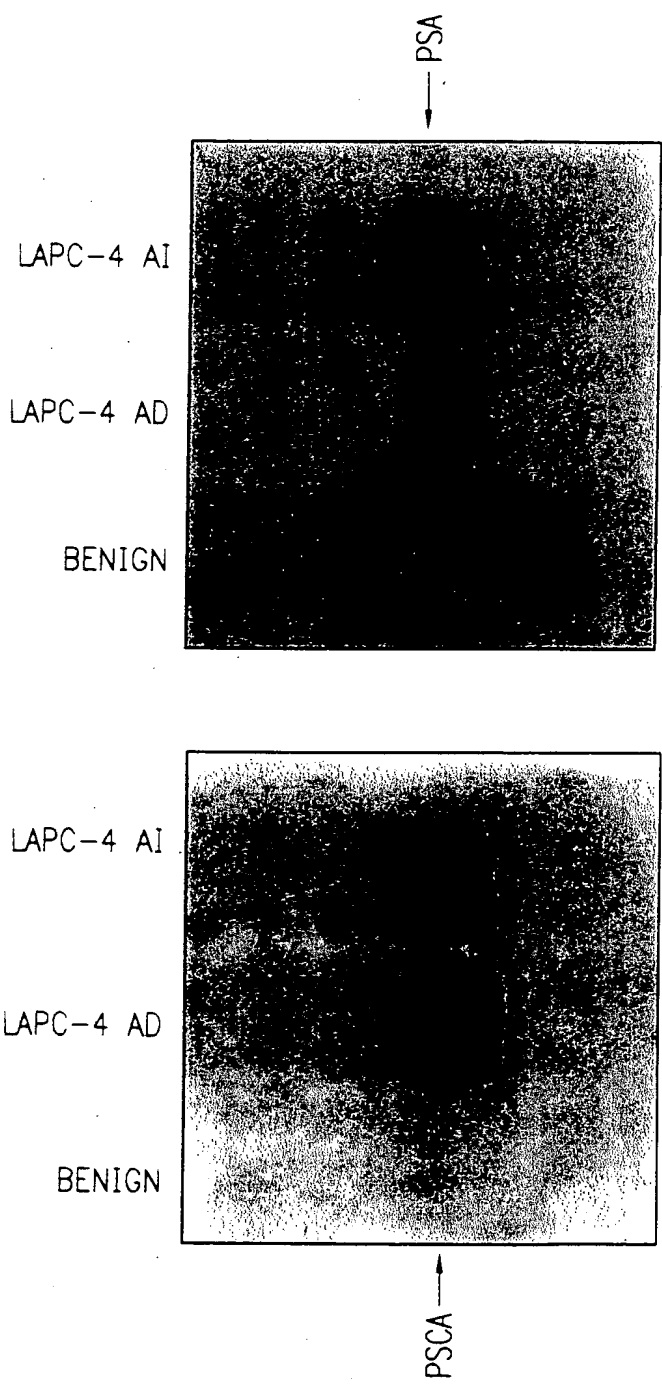


FIG. 9A

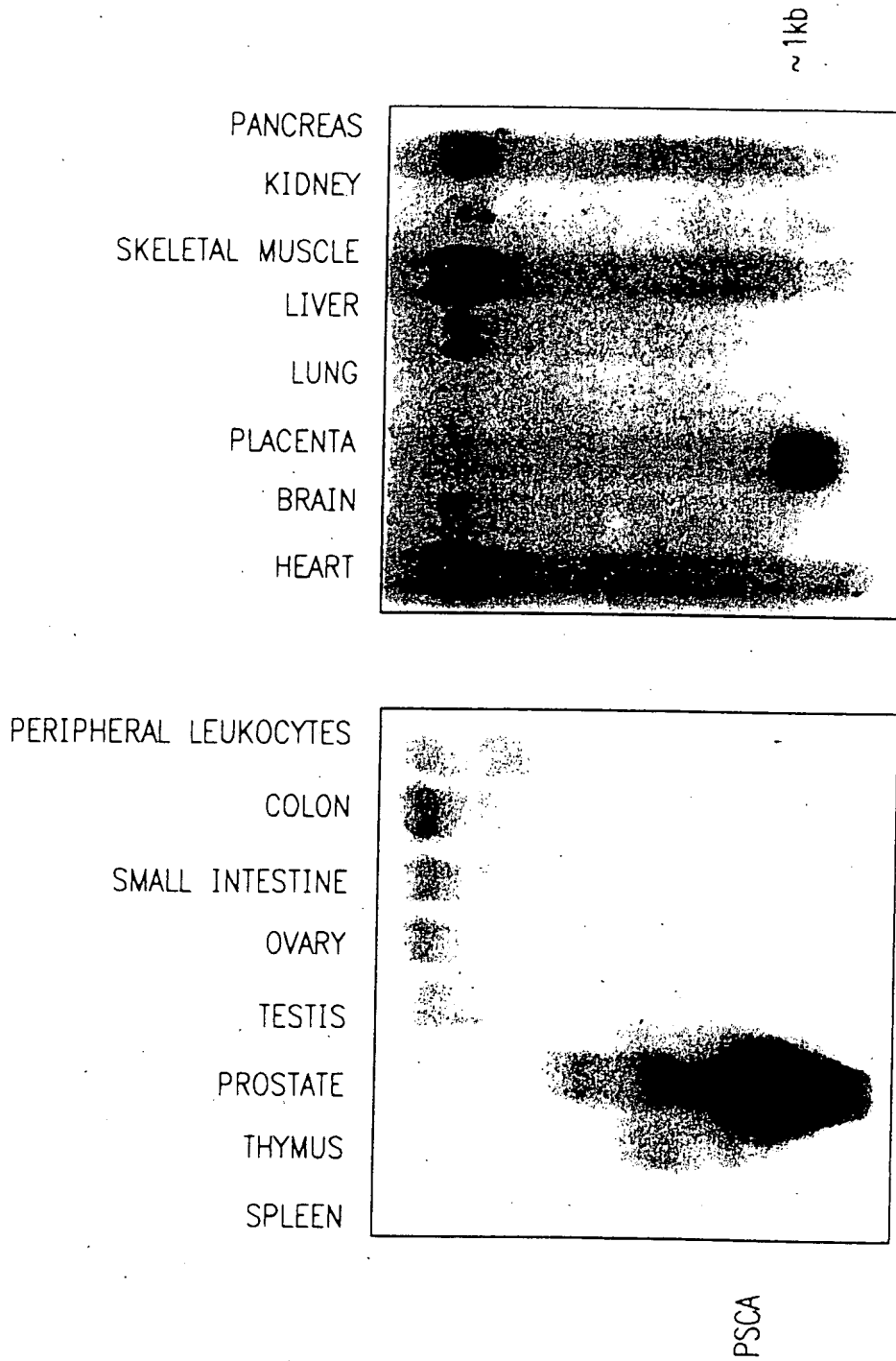


FIG. 9B

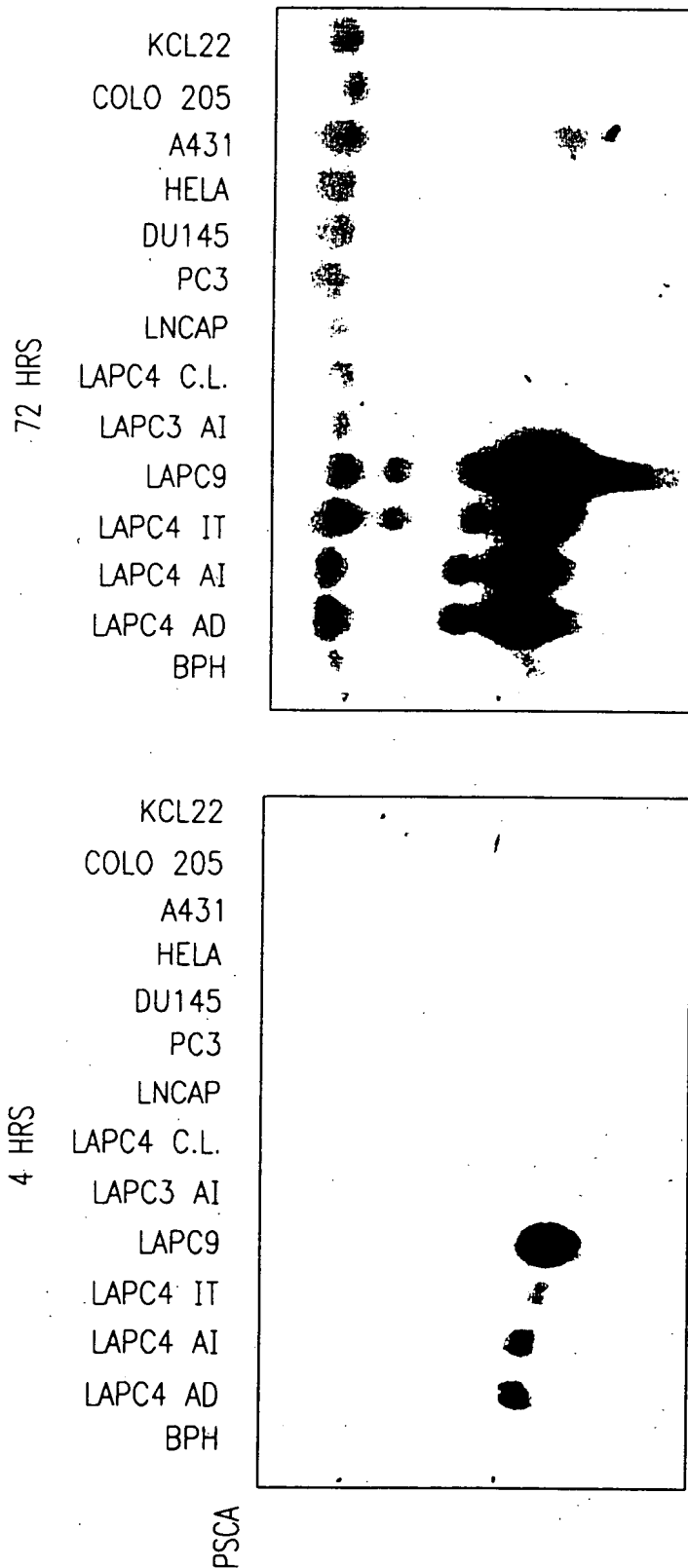
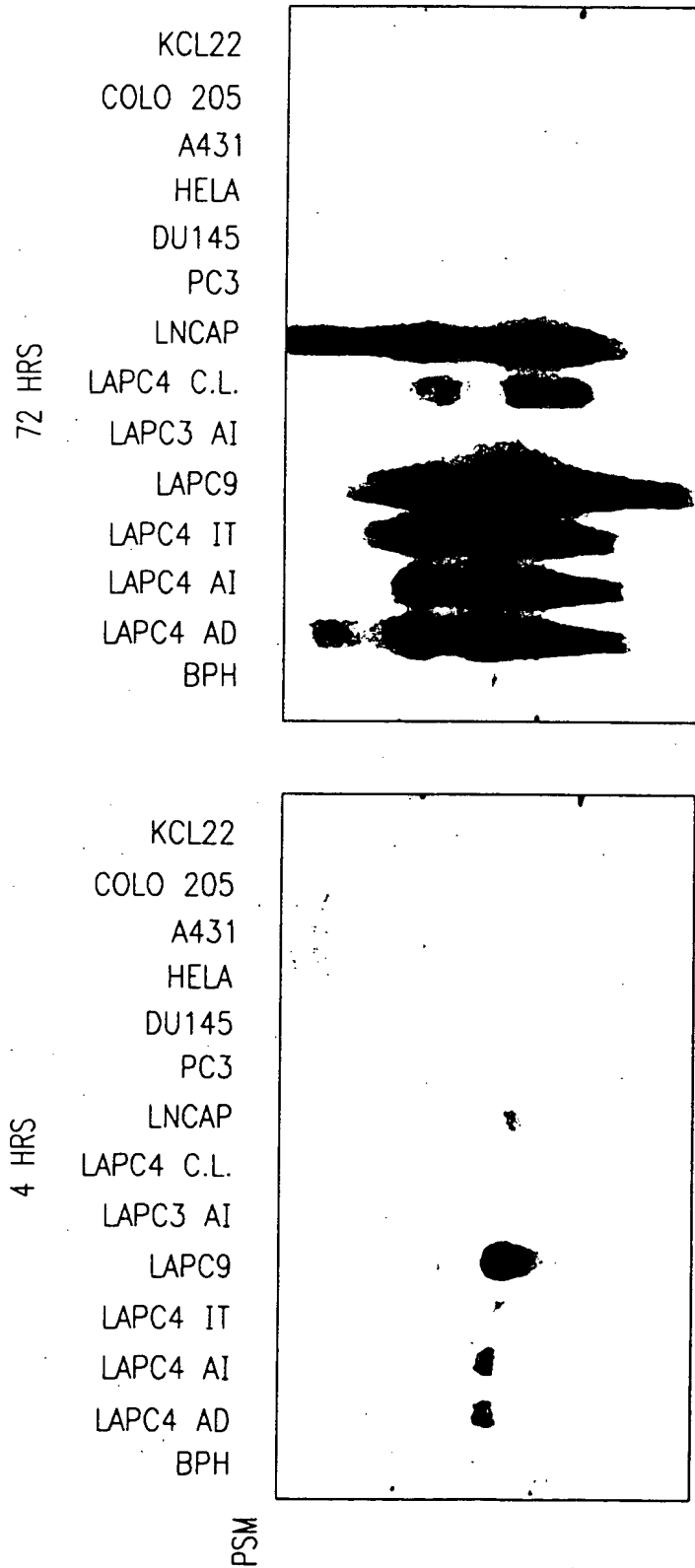
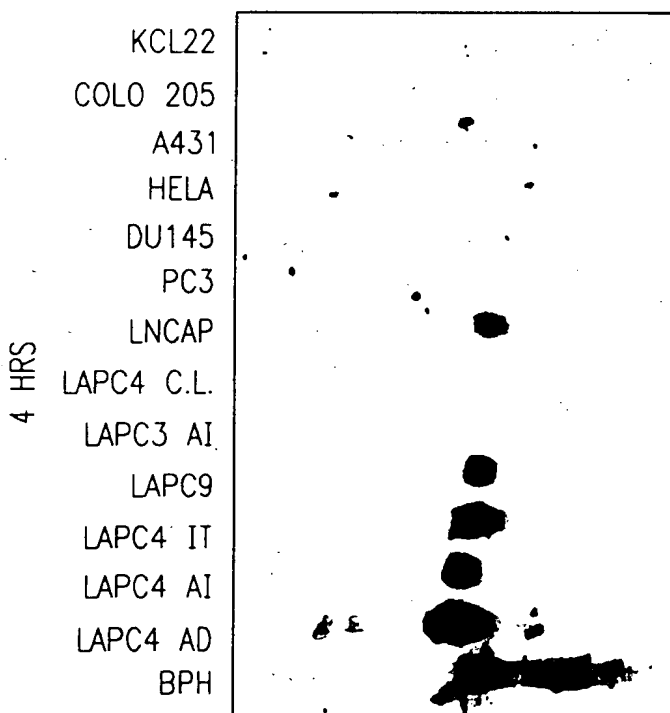
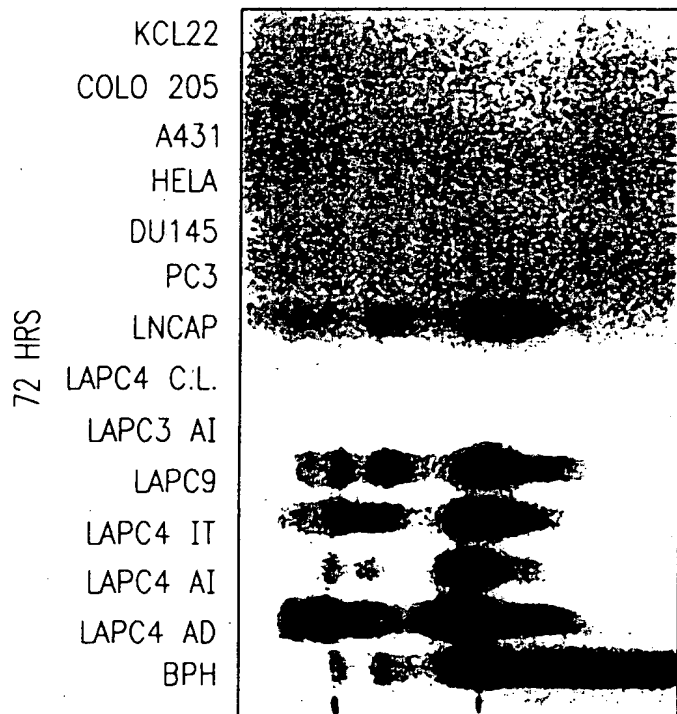


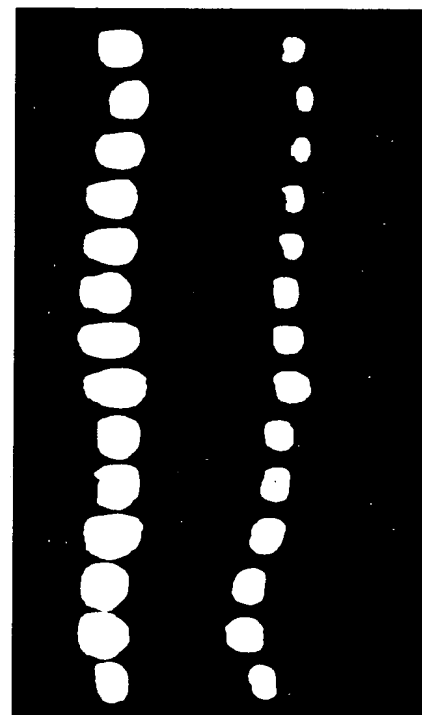
FIG. 10A

403620 8373360





PSA



ETBR

FIG. 10C

FIG. 11A

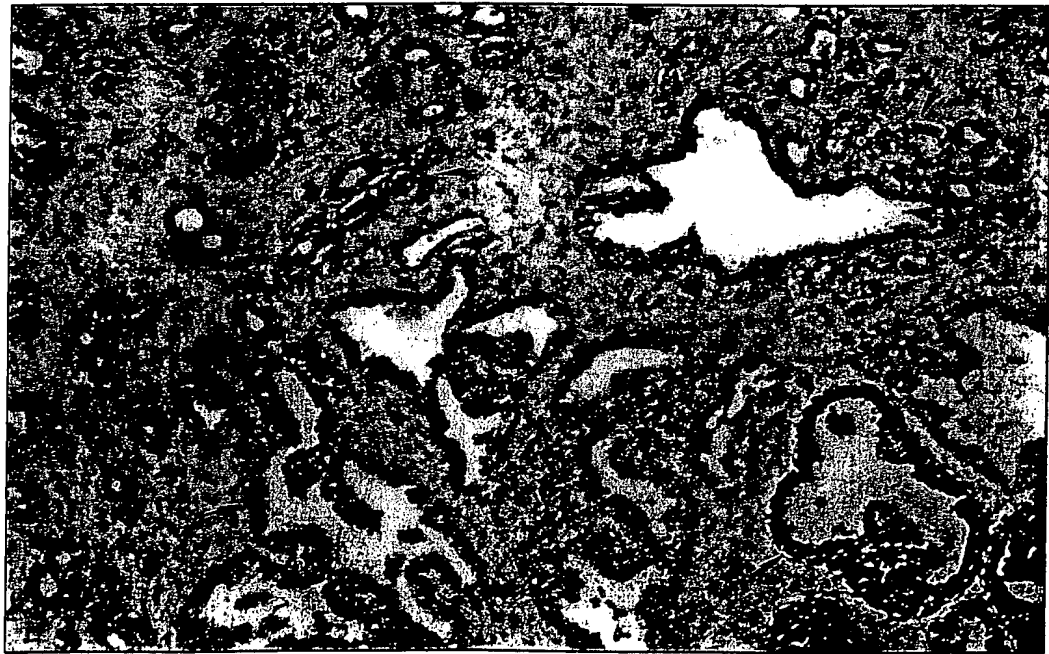


FIG. 11B

09855453.072604

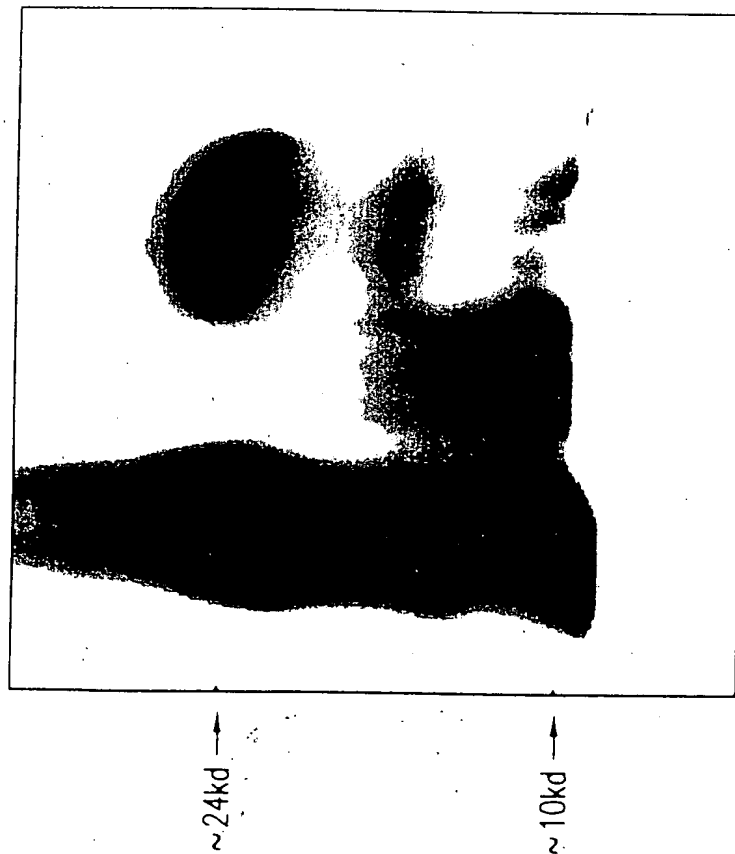
0955453.072504



FIG. 11C

FIG. 12A

O GLYCOSIDASE
N GLYCOSIDASE F
CONTROL



SECRETED
CELL ASSOCIATED

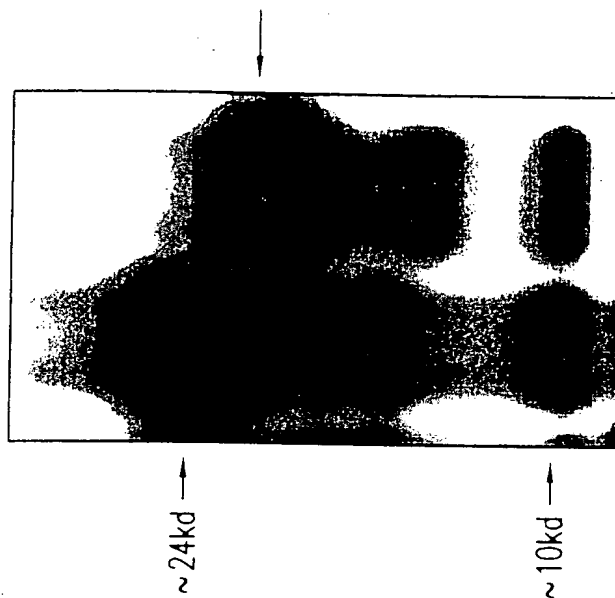


FIG. 12B

403320 6343360

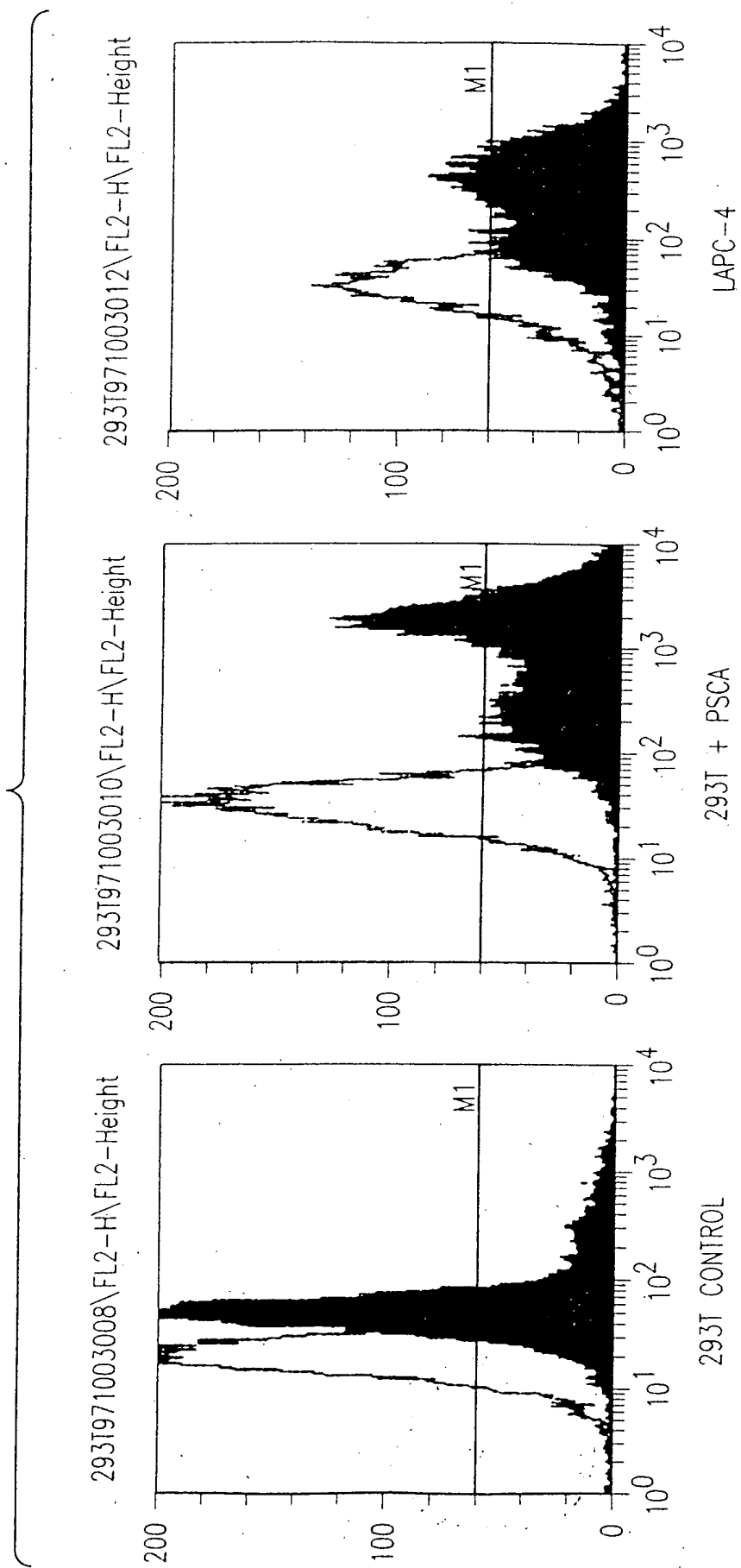
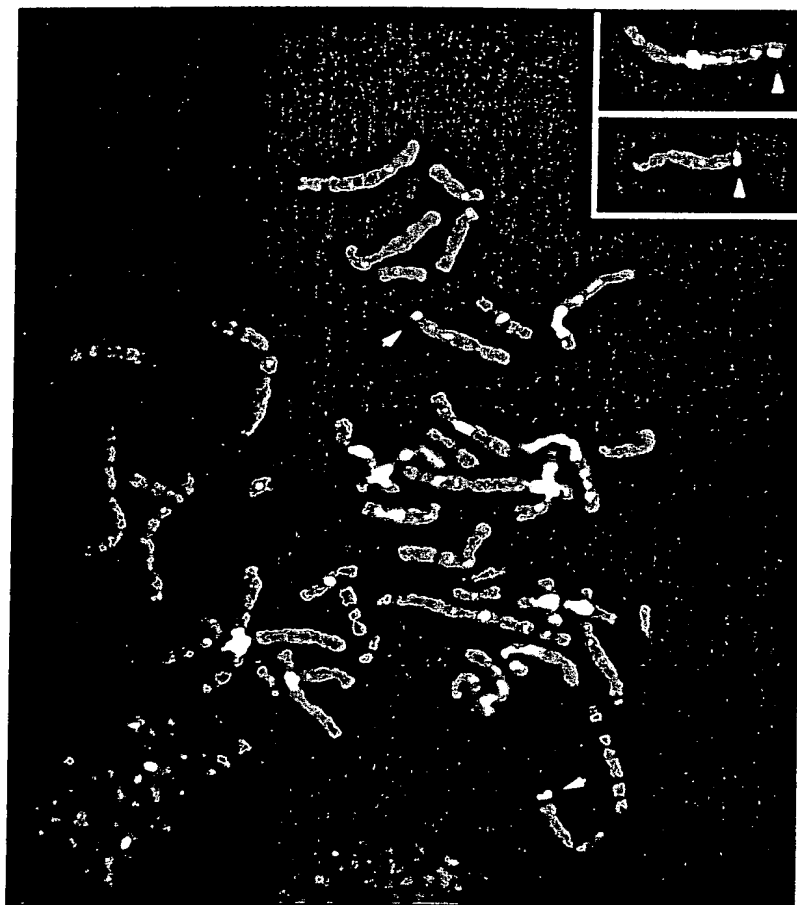


FIG. 12C

405220" 03755860

FIG. 13



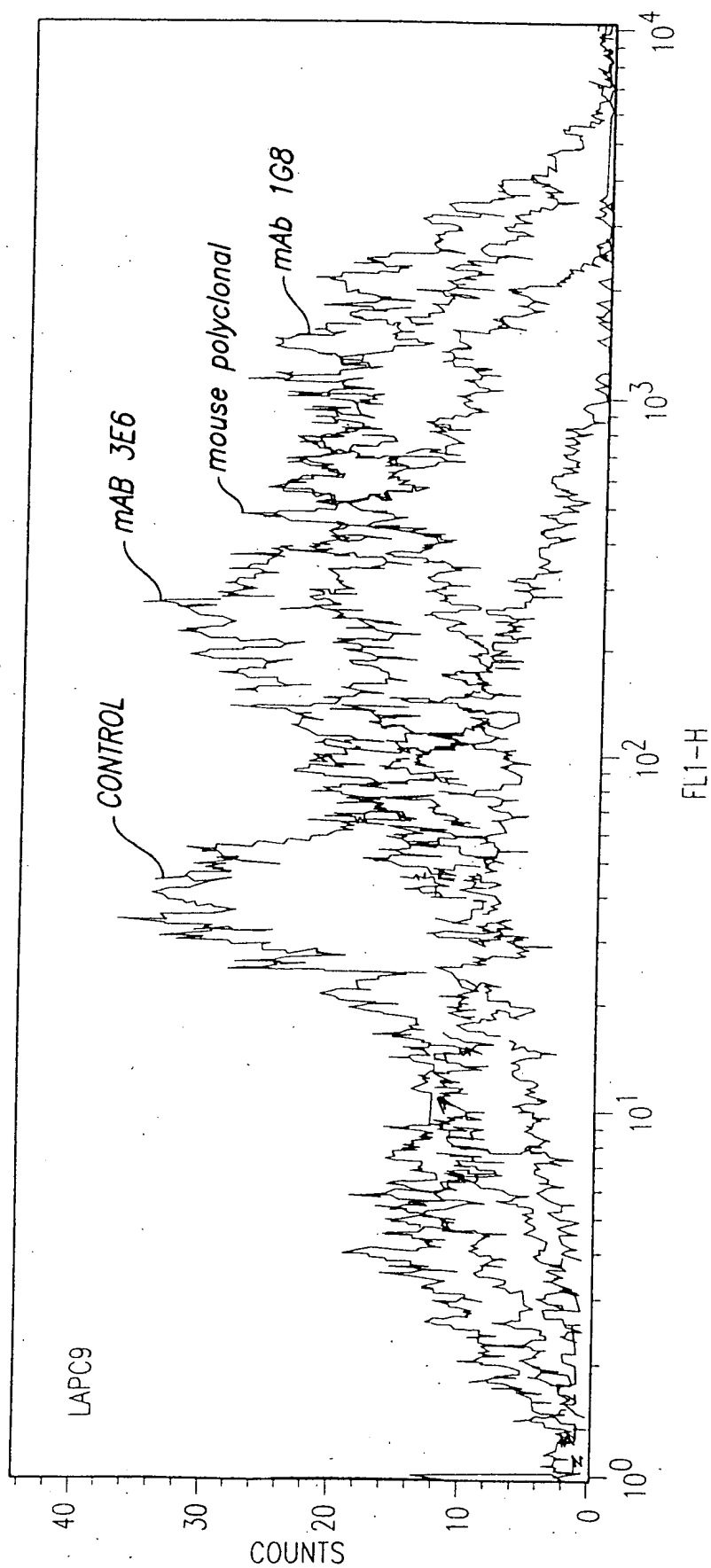


FIG. 14B

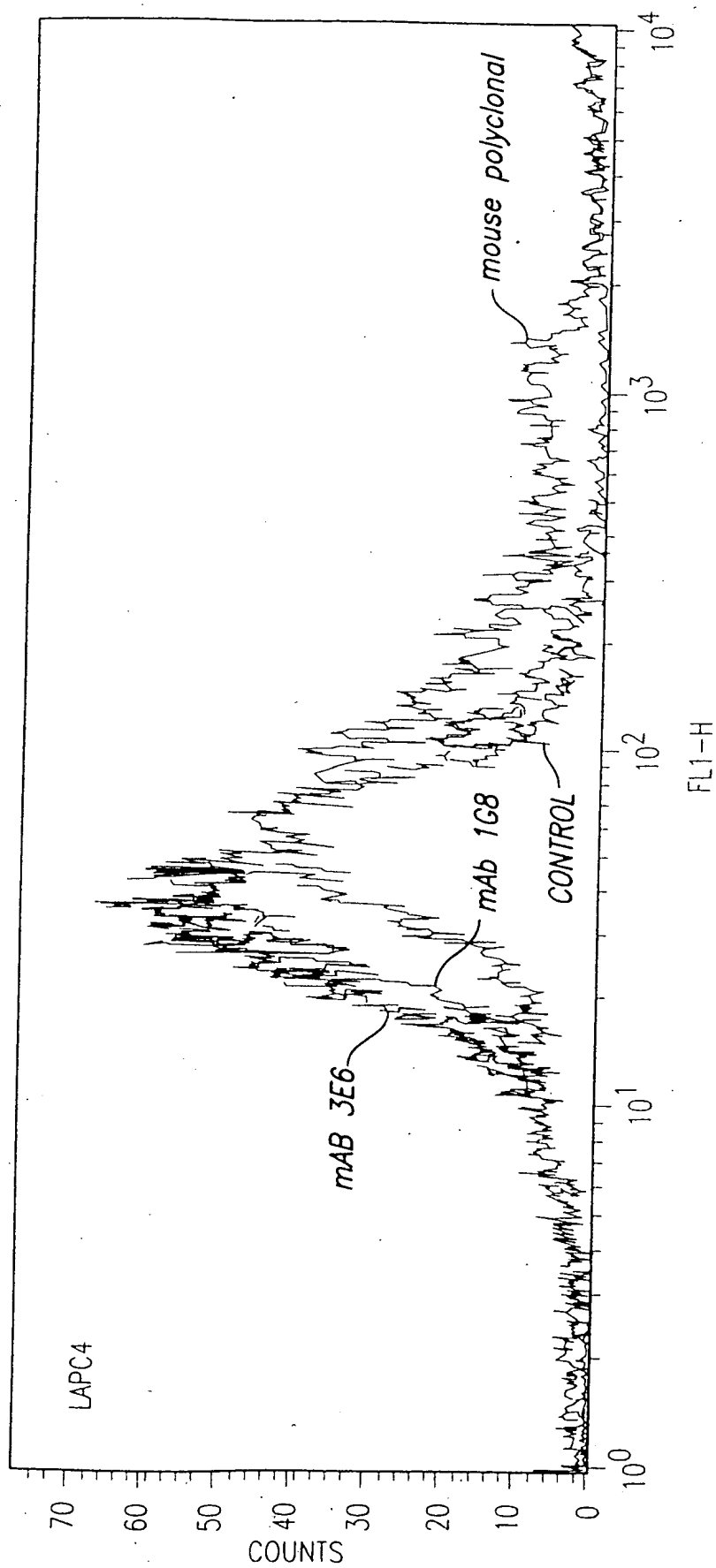
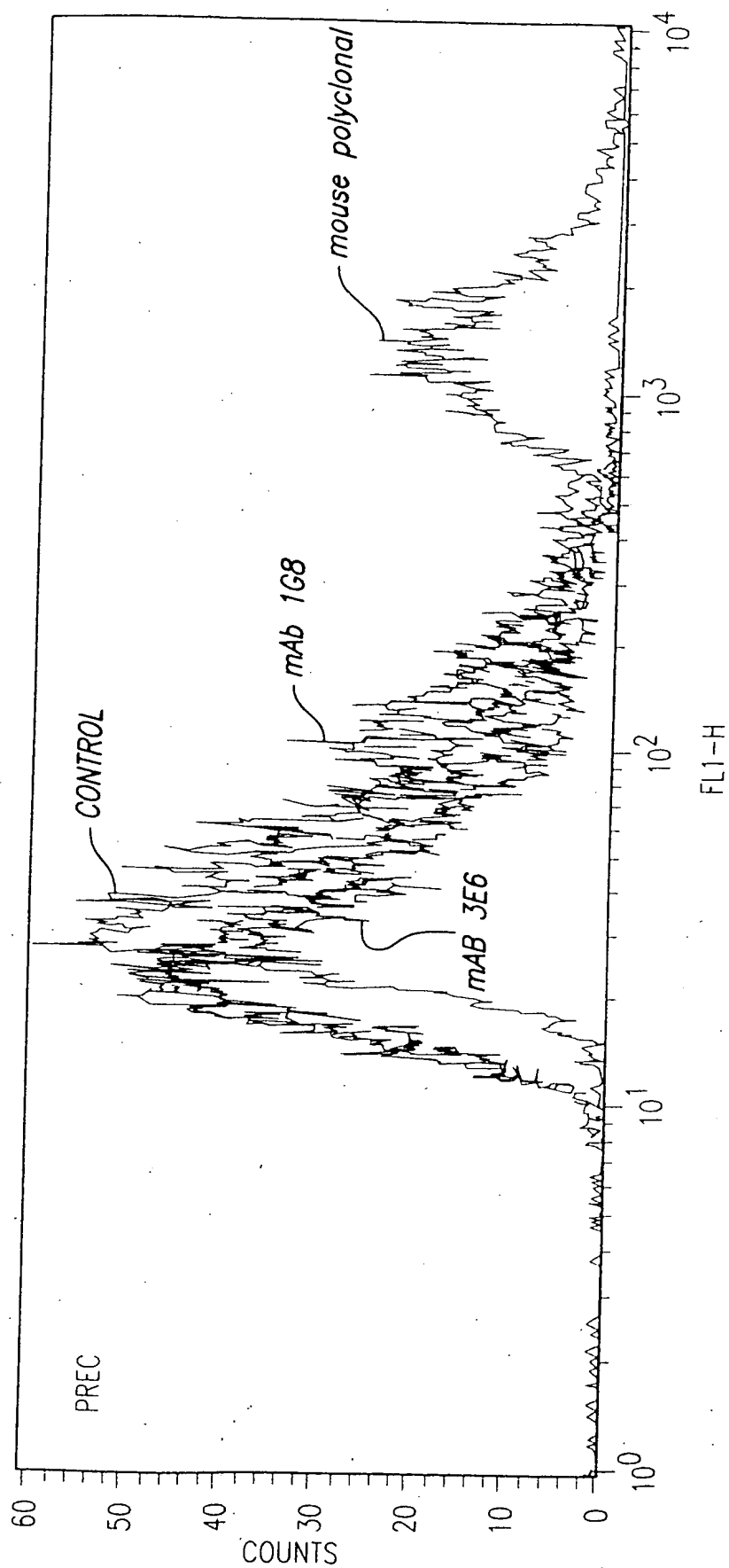


FIG. 14C



EPIIOPE MAP

mAb	ISOTYPE	FL (18-98)	N (2-50)	M (46-109)	C (85-123)
1G8	IgG1 k	2.039	0.007	0.628	0.000
2H9	IgG1 k	1.318	0.863	0.032	0.021
3C5	IgG2a k	2.893	1.965	0.016	0.005
3E6	IgG3 k	0.328	0.024	0.069	0.370
4A10	IgG2a k	2.039	1.315	0.000	0.014
2A2	IgG2a k	1.366	0.733	0.010	0.003
3G3	IgG2a k	2.805	1.731	0.004	0.000

FIG. 15A

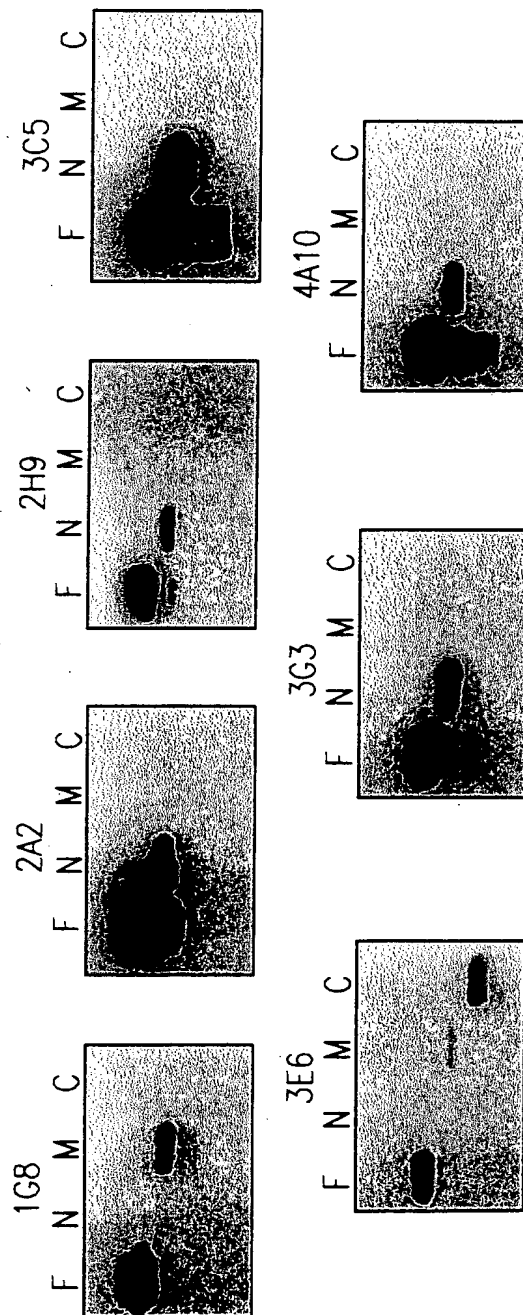


FIG. 15B

PROSTATE STEM CELL ANTIGEN (PSCA) IS A GPI-ANCHORED PROTEIN

1	M	K	I	F	L	P	V	L	L	A	A	L	L	G	V	E	R	A	S	S	hSCA-2
1	M	K	A	V	L	L	A	L	L	M	A	G	L	A	L	Q	P	G	T	A	hPSCA
1	M	K	T	V	L	F	L	L	L	A	T	Y	L	A	L	H	P	C	A	A	mPSCA
21	L	M	C	F	S	C	L	N	Q	K	S	N	L	Y	C	L	K	P	T	I	
21	L	L	C	Y	S	C	K	A	Q	V	S	N	E	D	C	L	Q	V	E	N*	
21	L	L	Q	C	Y	S	C	T	A	Q	M	N	N	R	D	C	L	N	V	Q	N*
41	C	S	D	Q	D	N	Y	C	V	T	V	S	A	S	A	G	I	G	N	L	
41	C	T	Q	L	G	E	Q	C	W	T	A	R	R	R	A	V	G	L	L	I	
41	C	S	L	D	Q	H	S	C	F	I	S	R	R	R	A	I	G	L	V	I	
61	V	T	F	G	H	S	L	S	K	T	C	S	P	A	C	P	I	P	E	G	
61	V	-	-	-	-	-	-	I	S	K	G	C	S	L	N	C	V	D	D	S	Q
61	V	-	-	-	-	-	-	I	S	K	G	C	S	S	Q	C	E	D	D	S	E
81	V	N	V	G	V	A	S	M	G	T	S	C	C	Q	Q	S	F	L	C	N*	F
76	D	Y	Y	V	G	K	K	-	N	T	T	G	G	D	T	D	L	C	N*	A	
76	N	Y	Y	L	G	K	K	-	N	T	T	C	C	Y	S	D	L	C	N*	V	
101	S	A	A	D	G	G	L	R	A	S	V	T	L	L	G	A	G	L	L	L	
95	S	C	A	H	A	L	Q	P	A	A	A	I	L	A	L	P	A	L	G	G	
95	N	G	A	H	T	L	K	P	P	T	T	L	G	L	L	T	V	L	C	S	
121	S	L	L	P	A	L	L	R	F	G	P	-	-	-	-	-	-	-	-	-	
115	L	L	L	W	G	P	G	Q	L	-	-	-	-	-	-	-	-	-	-	-	
115	L	L	L	W	G	S	S	R	L	-	-	-	-	-	-	-	-	-	-	-	

FIG. 16A

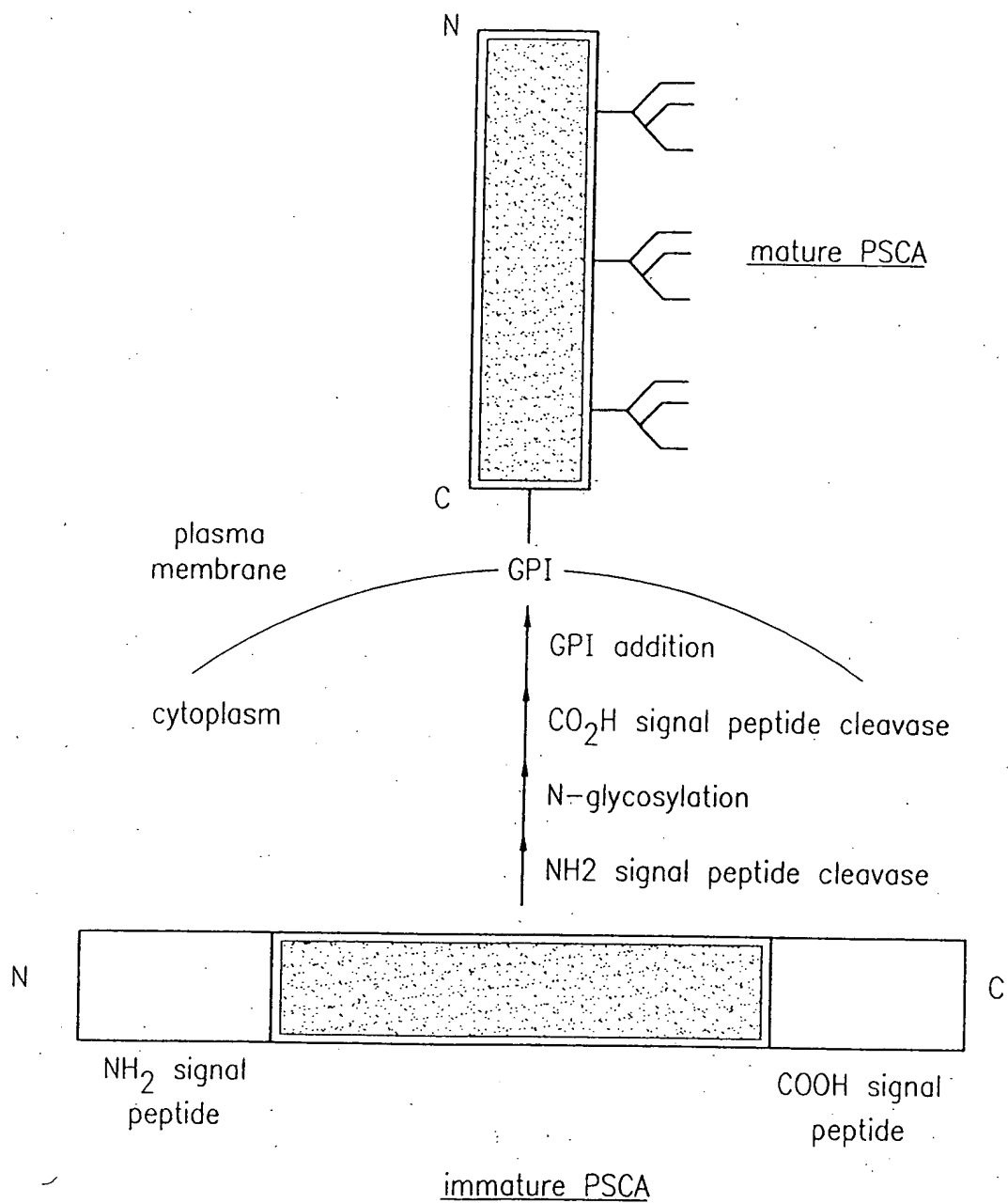
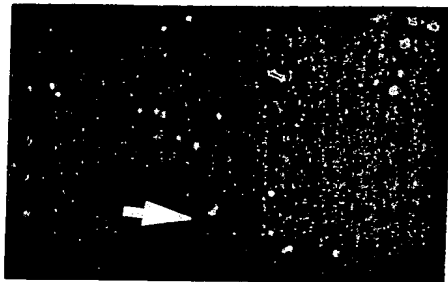


FIG. 16B

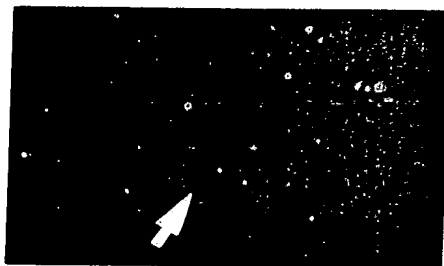
FIG. 17

GAIN CHROMOSOME 8

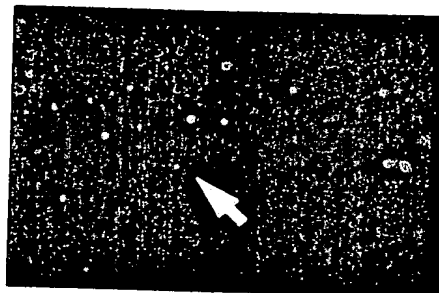


#34 c-myc

#34 PSCA



AMPLIFICATION



#75 c-myc

#75 PSCA

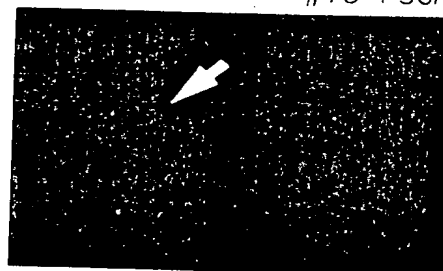


FIG. 18



A high-contrast, black and white image showing a dense, textured surface, possibly a rock or a piece of material, with a dark, irregular shape in the center. The image is heavily speckled and noisy, with a dark, irregular shape in the center that appears to be a shadow or a hole. The overall appearance is grainy and abstract, with no discernible text or figures.

FIG. 20

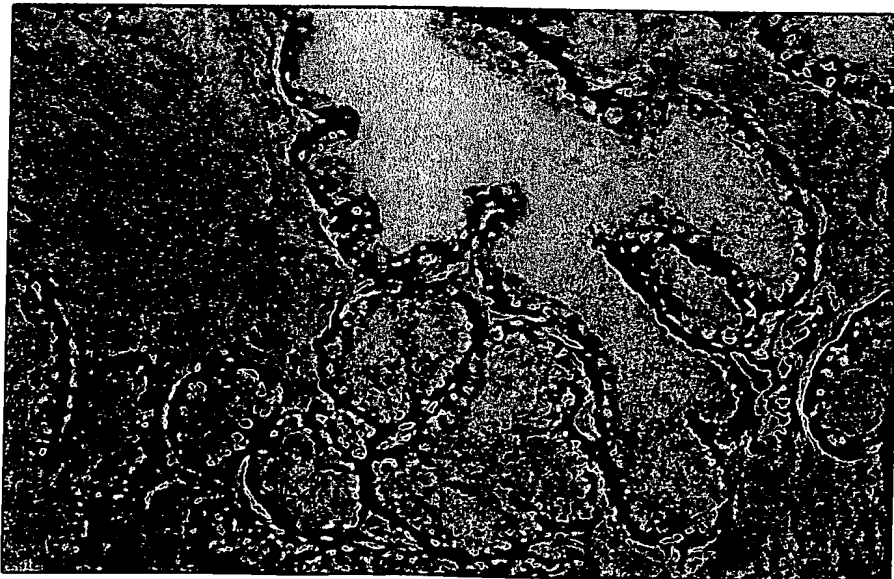
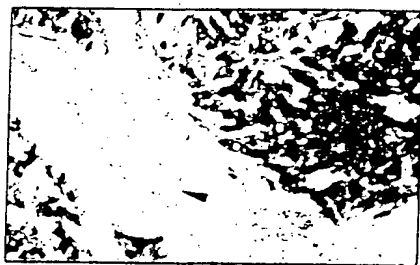
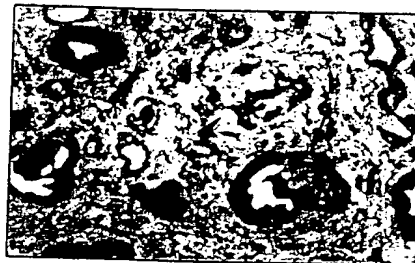


FIG. 21



patient 1:mAb 1G8



patient 2:mAb 1G8

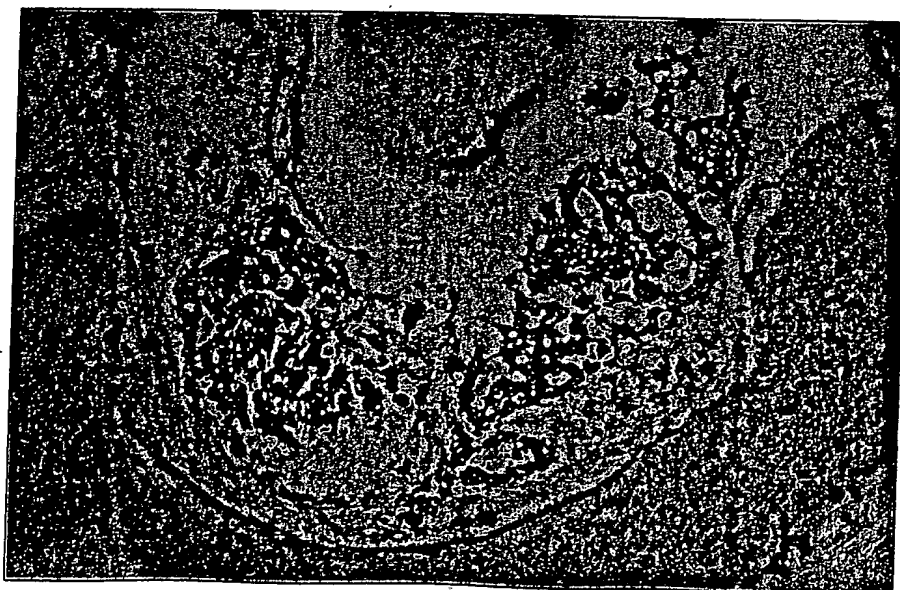


patient 3:mAb 1G8



patient 4:mAb 3E6

FIG. 22



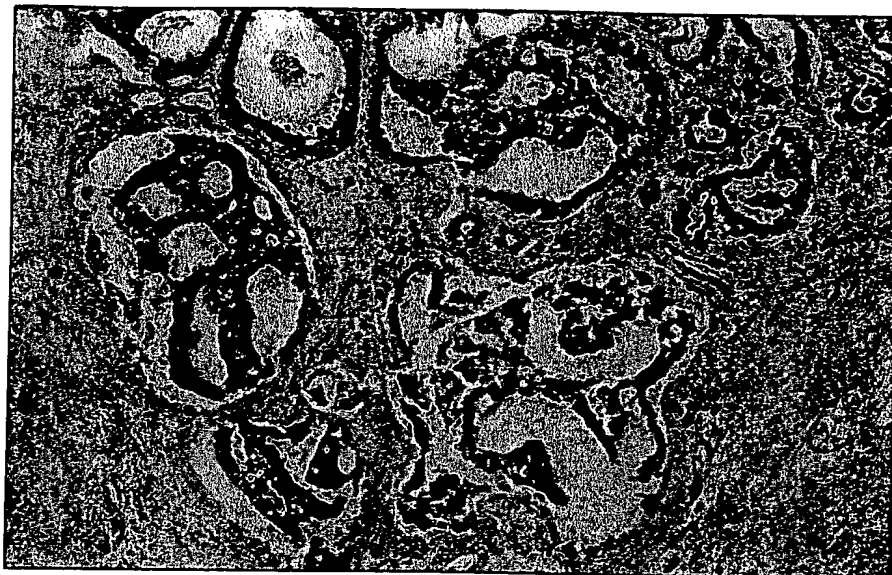


FIG. 23

FIG. 24



0055153 073504
105220 65455860

FIG. 25

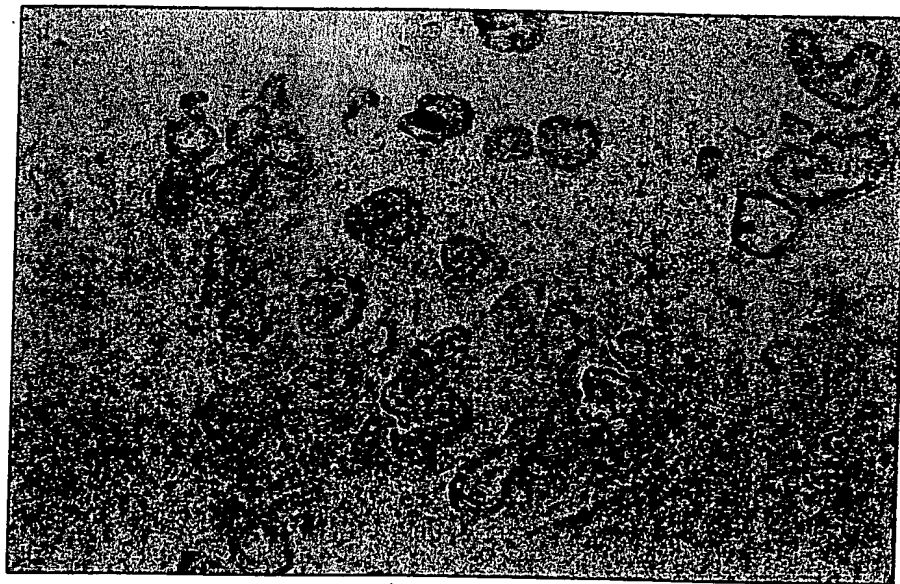
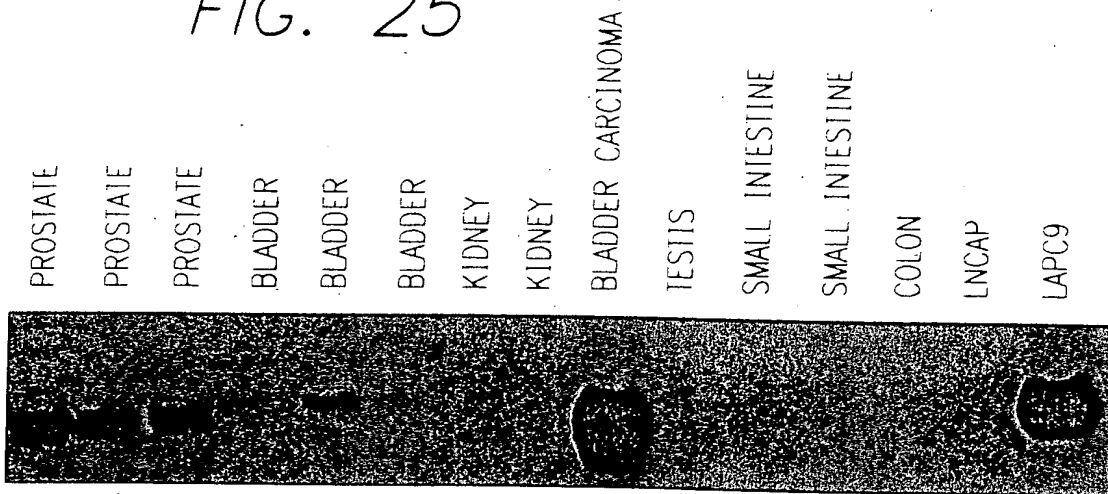


FIG. 26

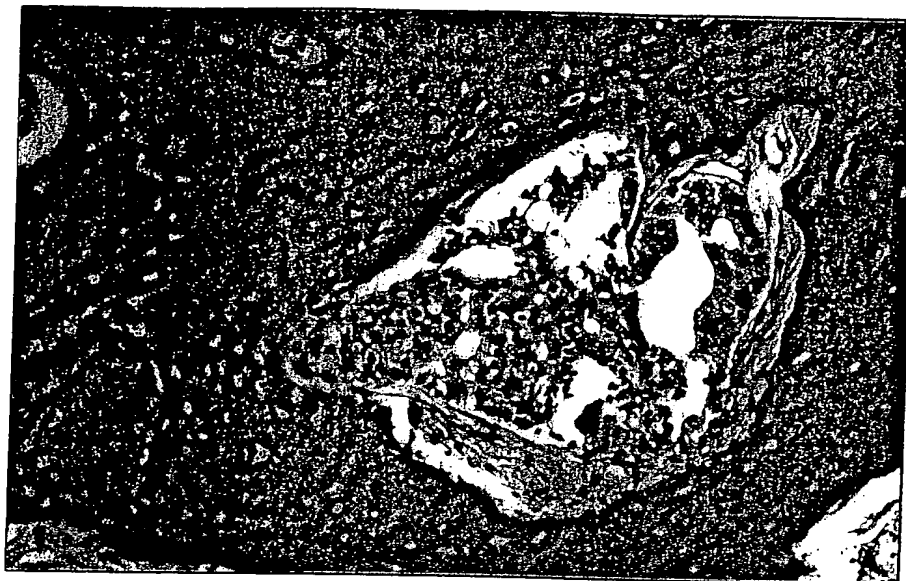
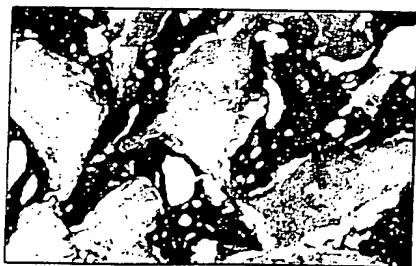


FIG. 27



Patient 5: H and E
and mAb 1G8



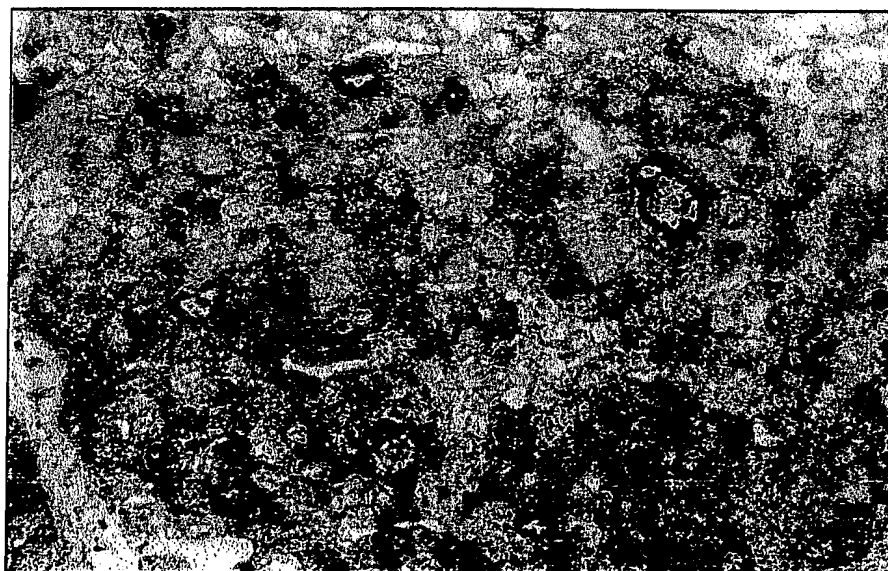
Patient 4: H and E
and mAb 3E6

FIG. 28



FIG. 29

FIG. 30



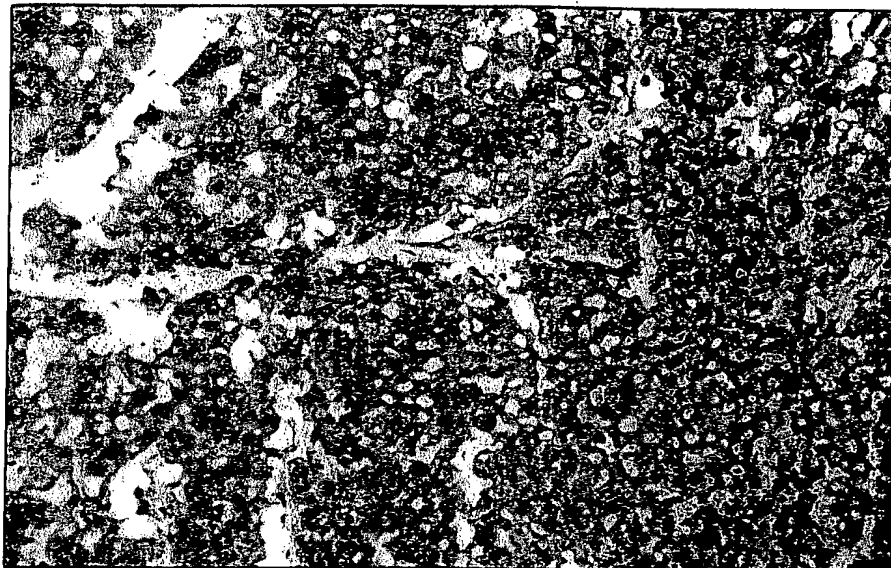


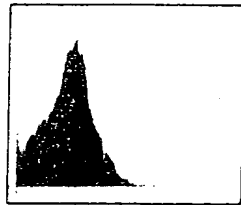
FIG. 31

FIG. 32

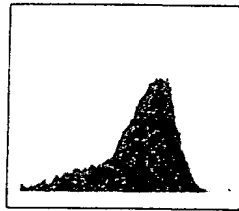


FIG. 33

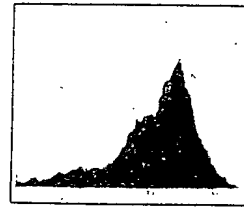
SECONDARY ANTIBODY



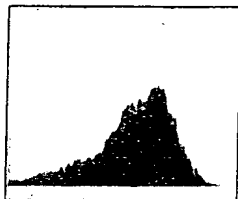
1G8



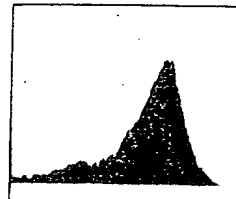
2H9



4A10



3C5



3E6

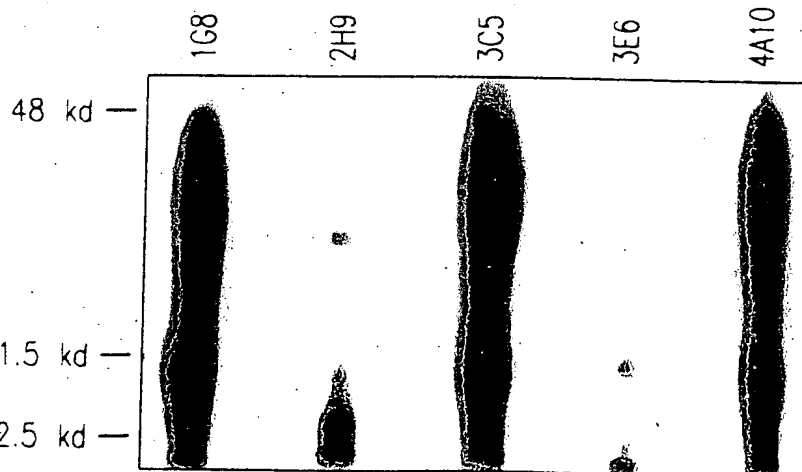
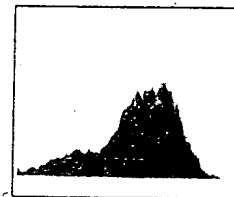


FIG. 34

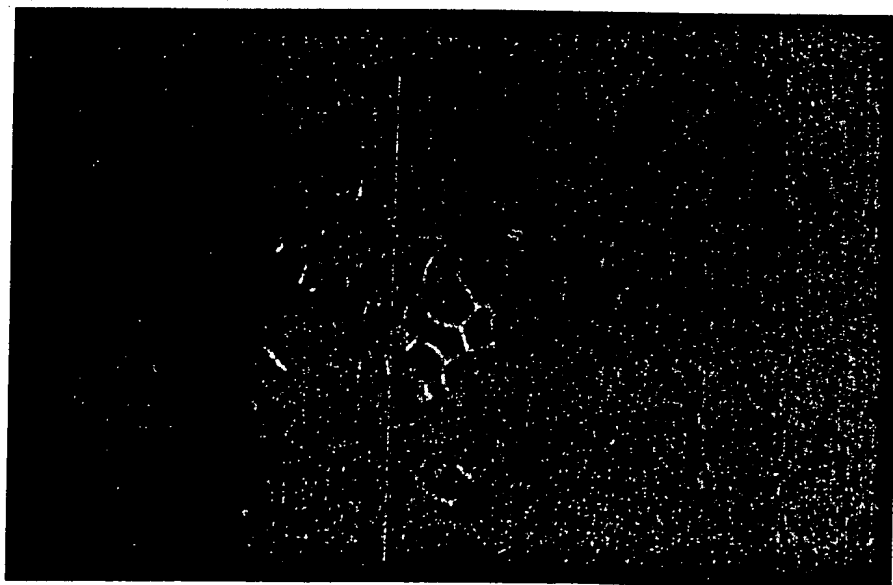
[illegible]

FIG. 36

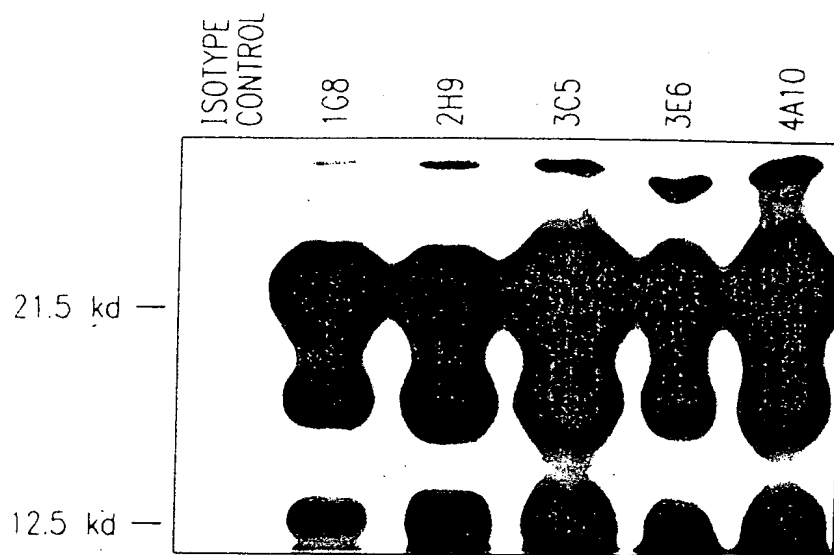


FIG. 37

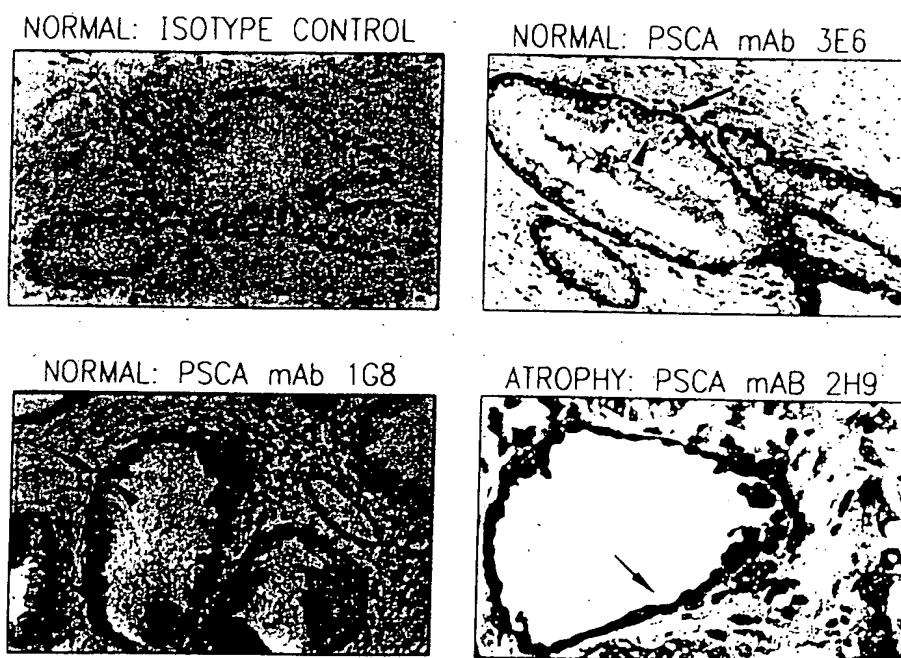


FIG. 38

FIG. 40A

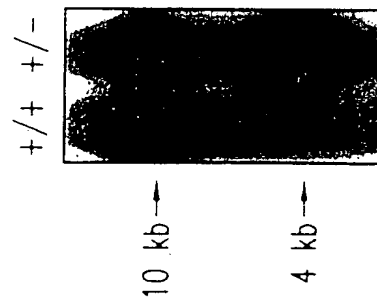
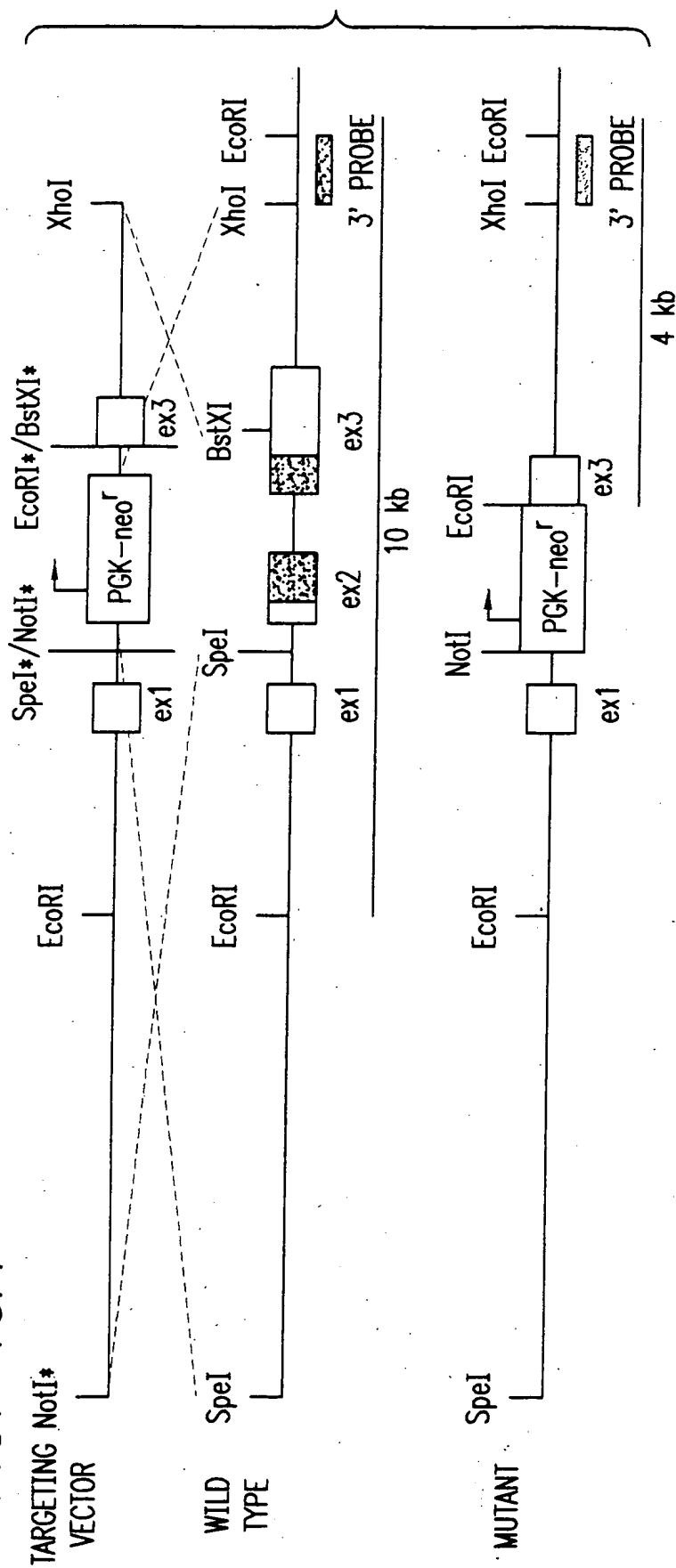
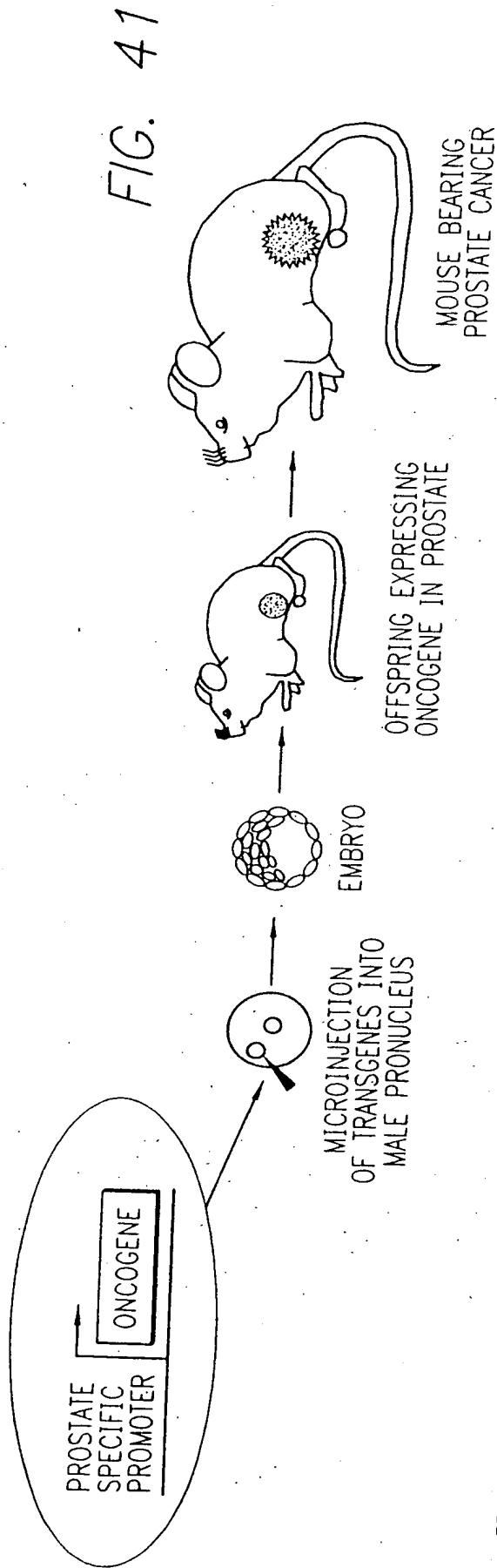


FIG. 40B



TRANSGENE	TARGET TISSUES	CHARACTERISTICS
C3(1) (~3 kb)/ SV40 LARGE+SMALL, T MAROULAKOU et al. 1994 PNAS	PROSTATE (SECRETORY CELLS) URETHRAL, MAMMARY AND SWEAT GLAND	LOW-GRADE PIN 8-12 WKS HIGH-GRADE PIN 8-12 WKS INVASIVE CARCINOMA 28 WKS NO METASTASES
PROBASIN (~426 bp)/ SV40 LARGE+SMALL, T GREENBERG et al. 1995 PNAS	PROSTATE (SECRETORY CELLS)	LOW-GRADE PIN 5-8 WKS HIGH-GRADE PIN 8-12 WKS INVASIVE CARCINOMA 12 WKS METASTASES IN LYMPH NODE, LUNG, LIVER AND BONE
CRYPTIDIN2 (~6.5 kb)/ SV40 LARGE+SMALL, T GARABEDIAN et al. 1998 PNAS	PROSTATE (NEUROENDOCRINE CELLS) SMALL INTESTINE	LOW-GRADE PIN 8-12 WKS HIGH-GRADE PIN 8-12 WKS INVASIVE CARCINOMA 16 WKS METASTASES IN LYMPH NODE, LUNG, LIVER, AND BONE

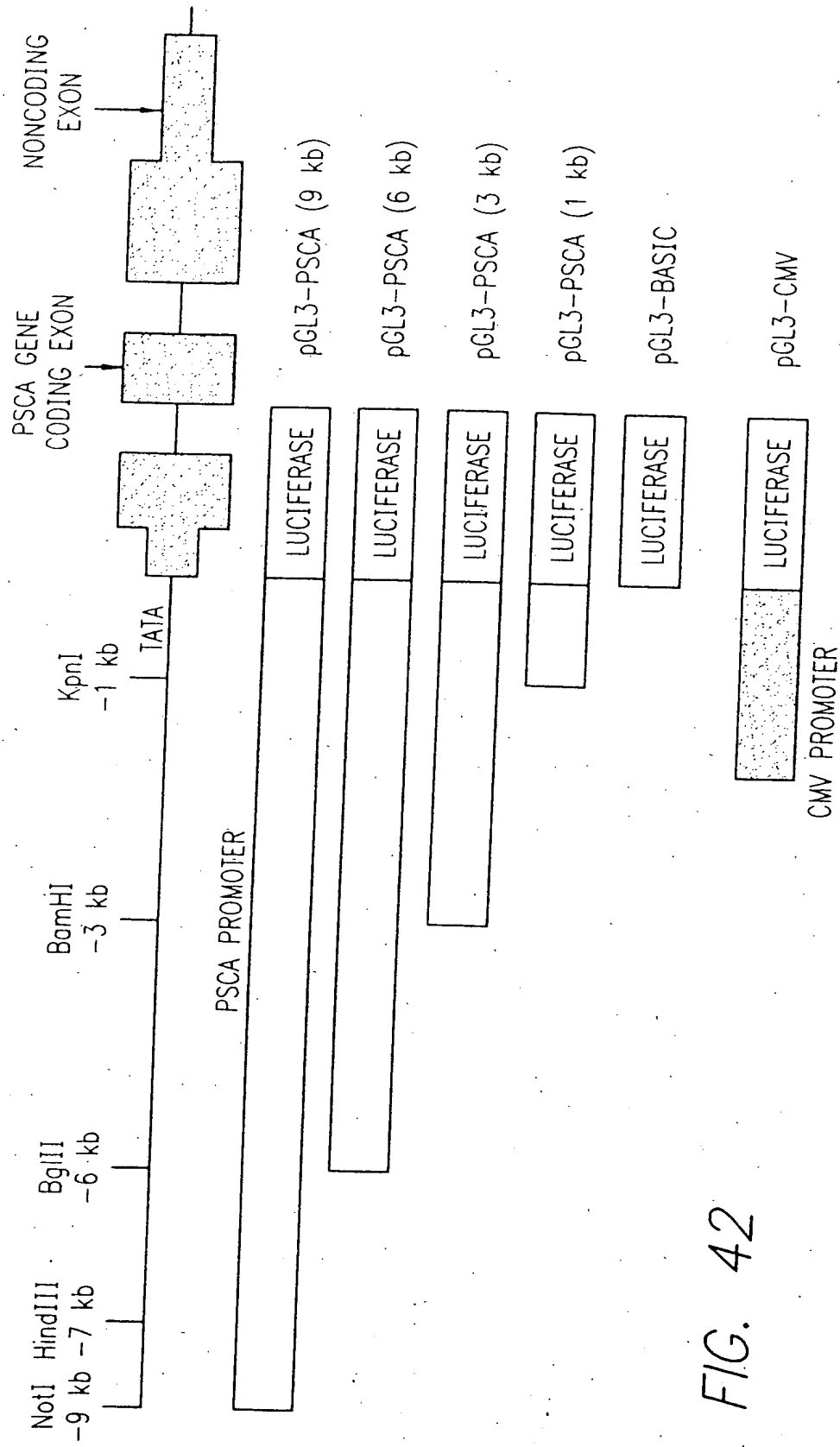


FIG. 42

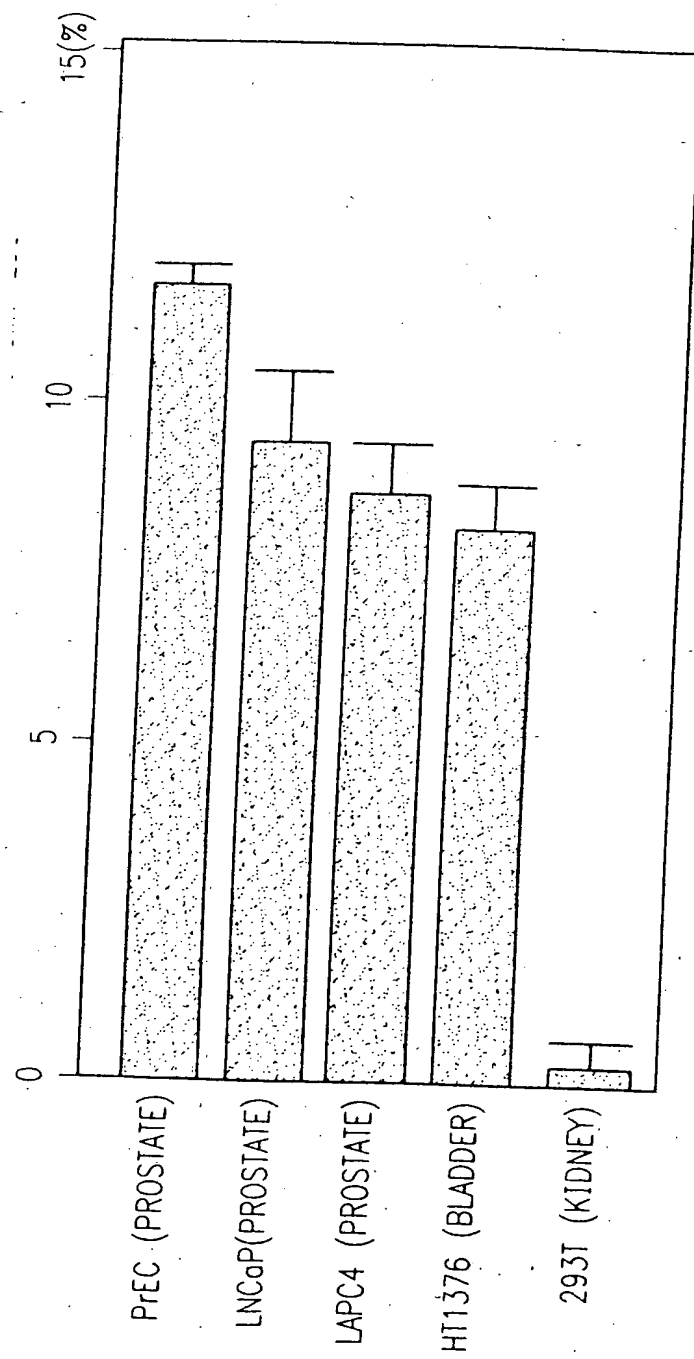


FIG. 43

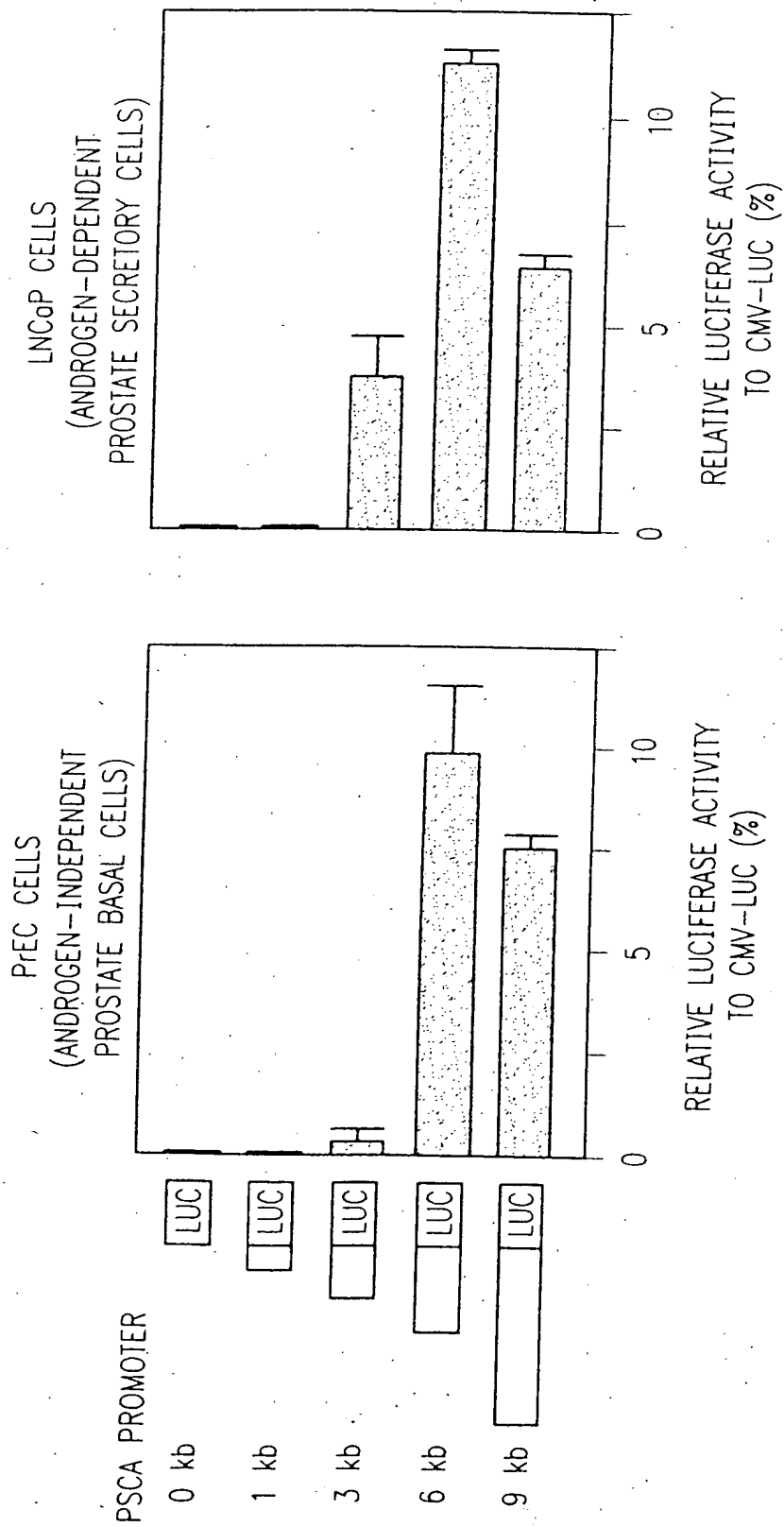
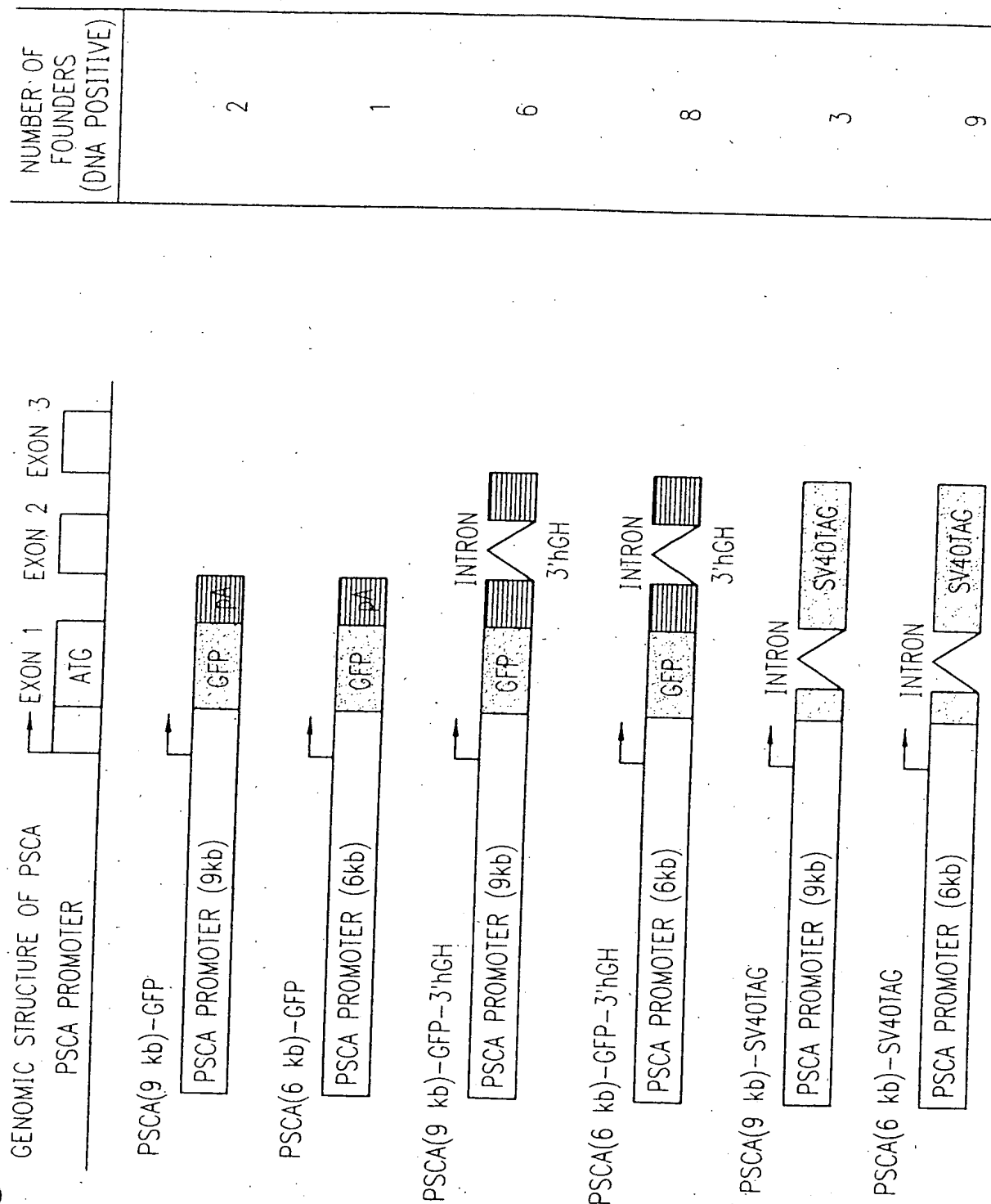


FIG. 44

FIG. 45



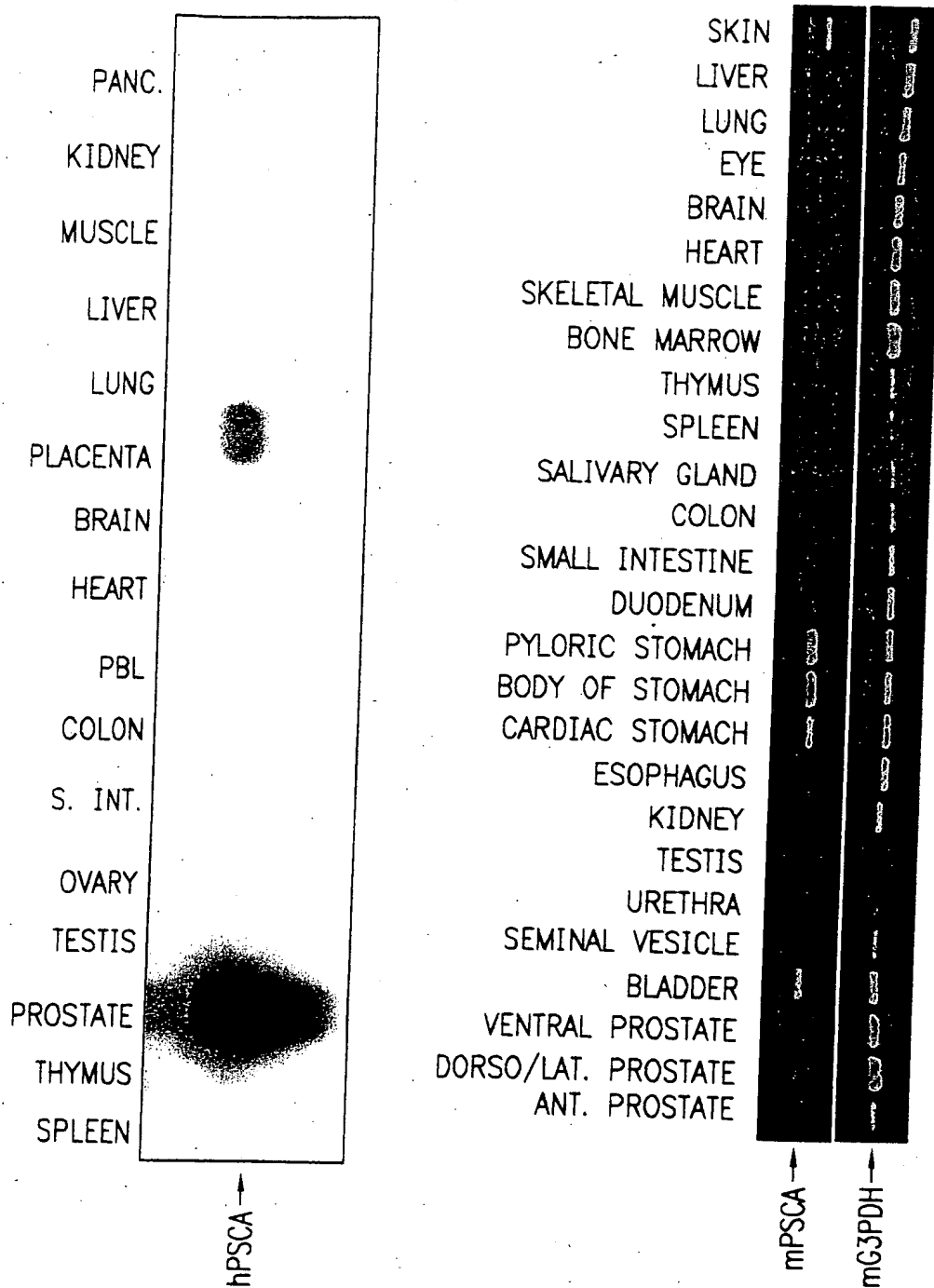
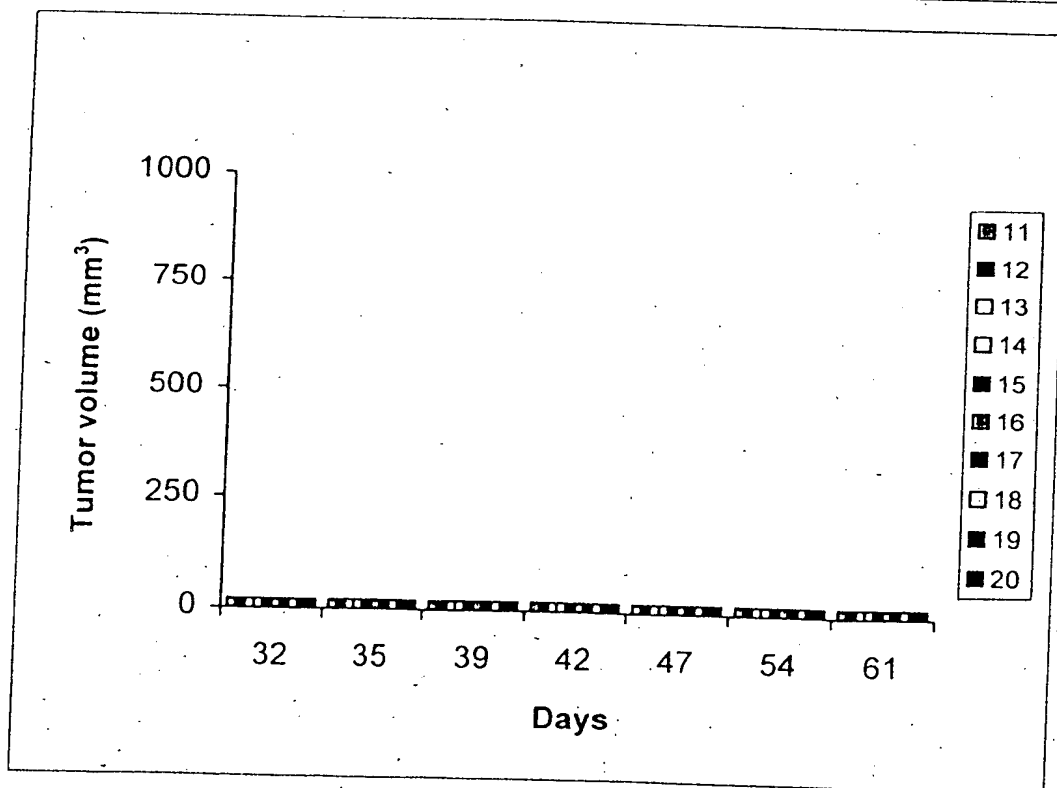
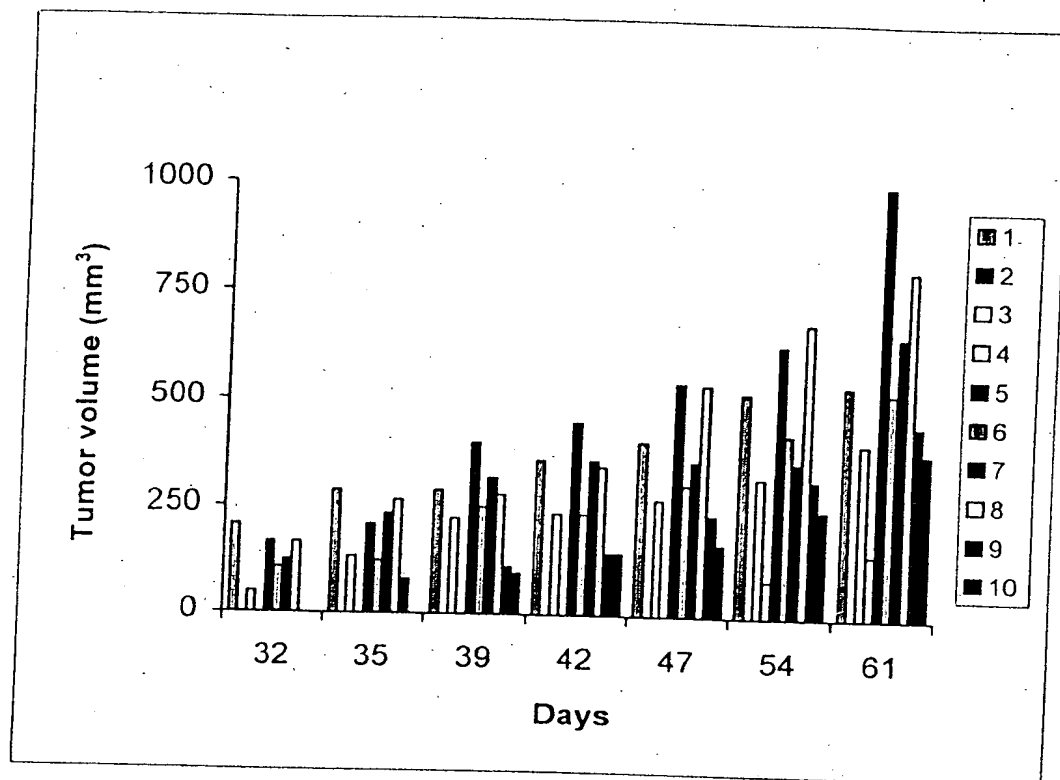


FIG. 47

FIG. 48



20220125155859

FIG. 49

A

Epitope recognized (OD 450 nm)

<u>mAb</u>	<u>Isotype</u>	<u>F (18-98)</u>	<u>N (2-50)</u>	<u>M (46-109)</u>	<u>C (85-123)</u>
1G8	IgG1 k	1.485	0.004	1.273	0.003
2A2	IgG2a k	0.973	0.631	0.023	0.010
2H9	IgG1 k	1.069	1.026	0.002	0.001
3C5	IgG2a k	1.916	1.709	0.006	0.002
3E6	IgG3 k	1.609	0.036	1.133	2.118
3G3	IgG2a k	2.805	1.731	0.004	0.000
4A10	IgG2a k	1.053	0.493	0.000	0.001

B

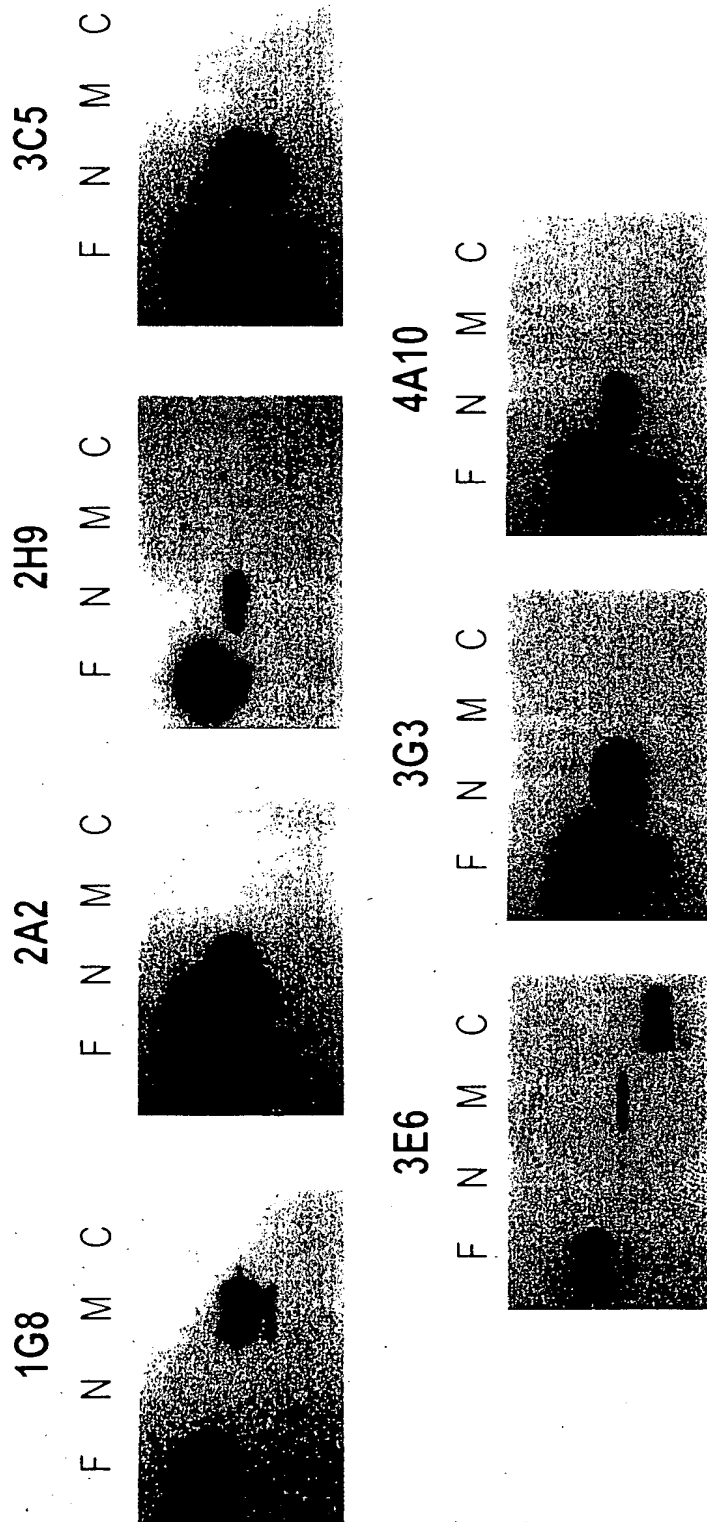
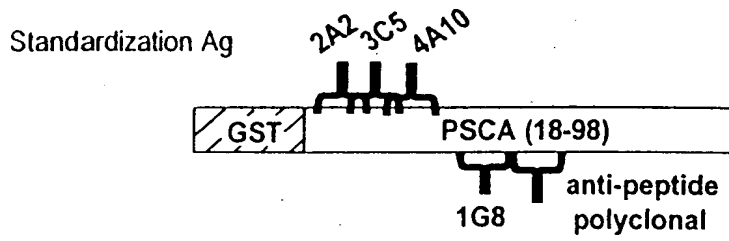
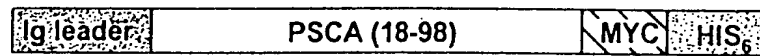


FIG. 50

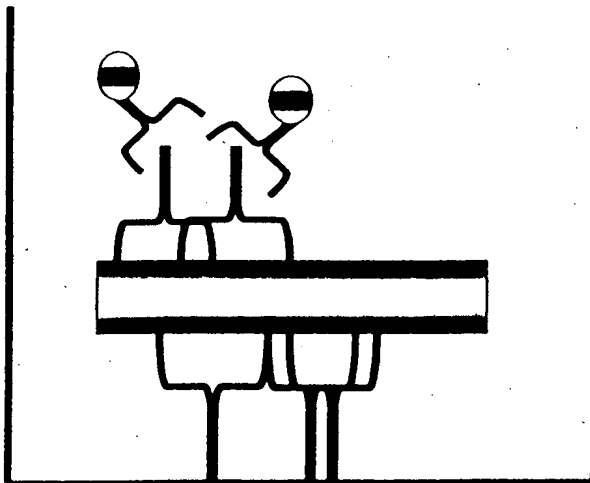
A



Engineered mammalian secreted form



B



Anti-IgG2a HRP

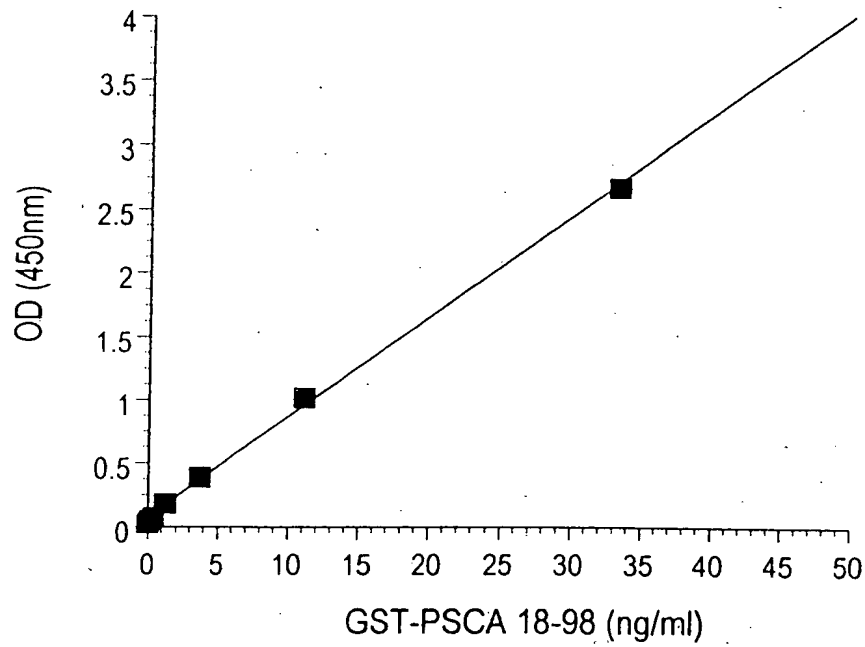
Anti-PSCA mAbs 3C5+4A10+2A2 (IgG2a)

PSCA

Affinity purified anti-peptide polyclonal
+ mAb 1G8 (IgG1)

FIG. 51

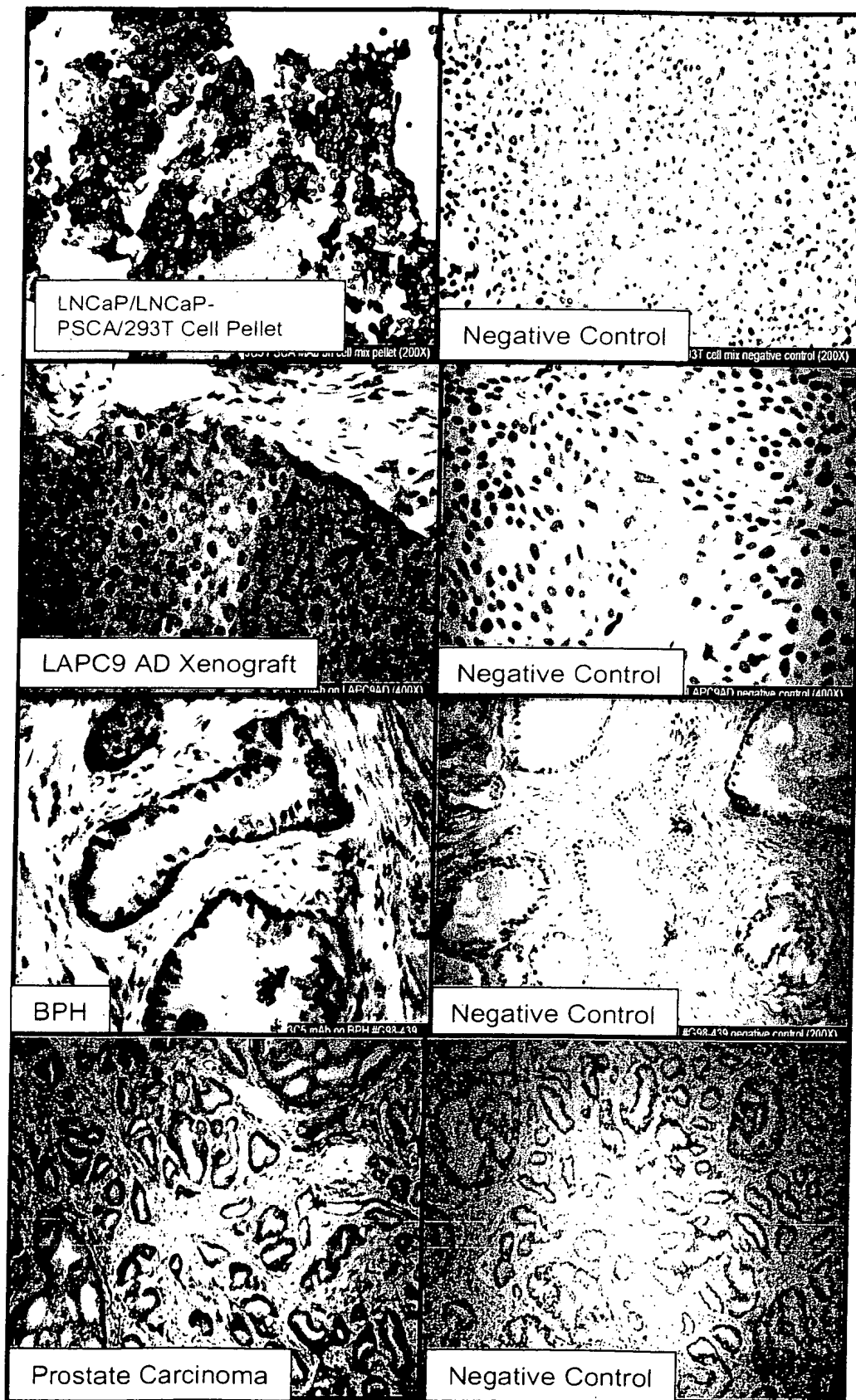
A



B

Sample	OD+range (n=2)	ng/ml
vector	0.005+0.001	ND
vector+hu serum	0.004+0.001	ND
secPSCA	2.695+0.031	32.92
secPSCA+hu serum	2.187+0.029	26.55

FIG. 52



0055453 072504

FIG. 53

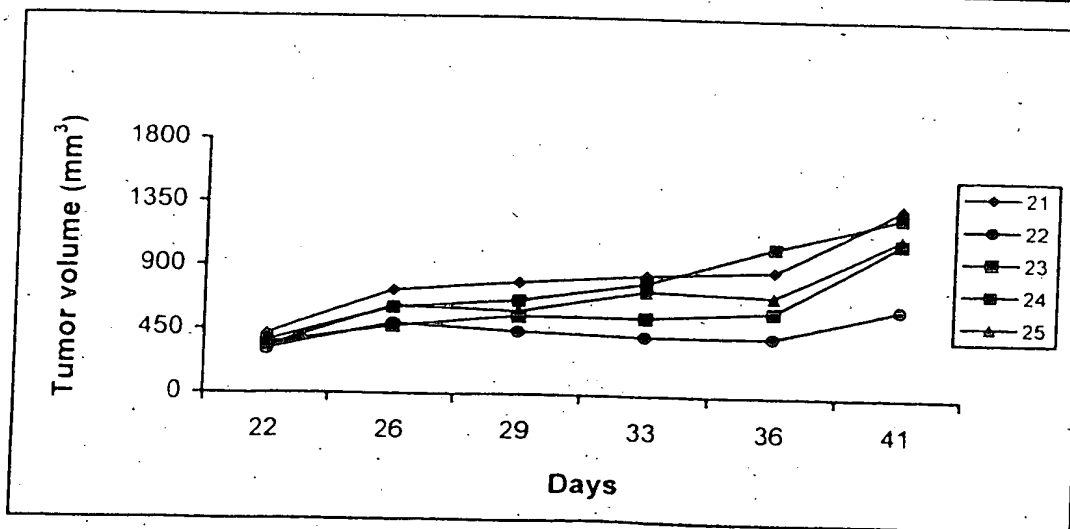
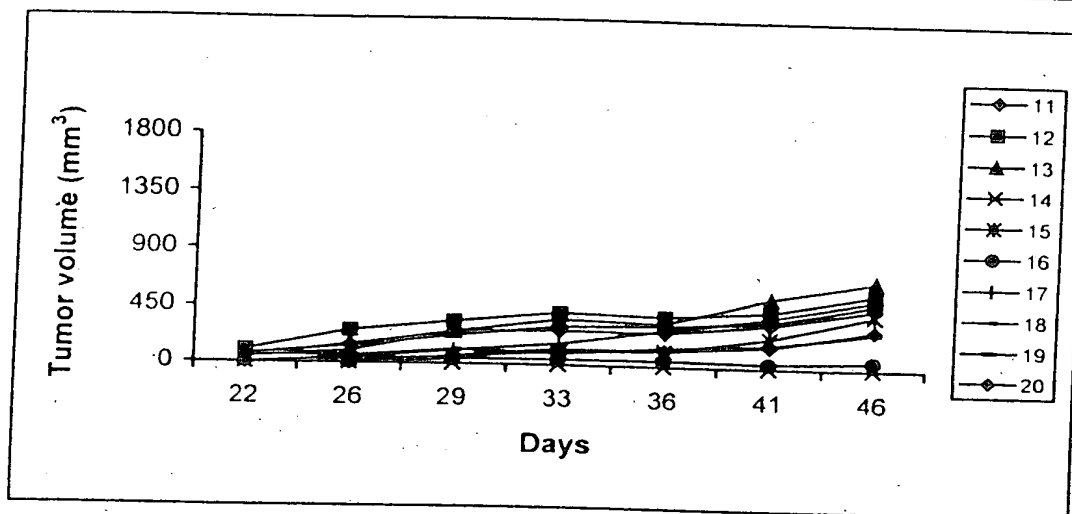
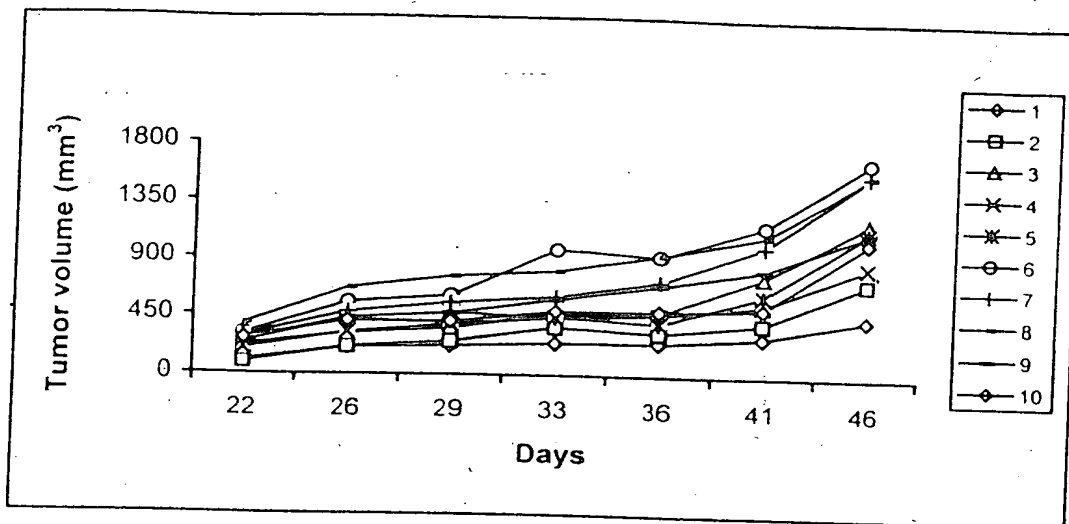


FIG. 54

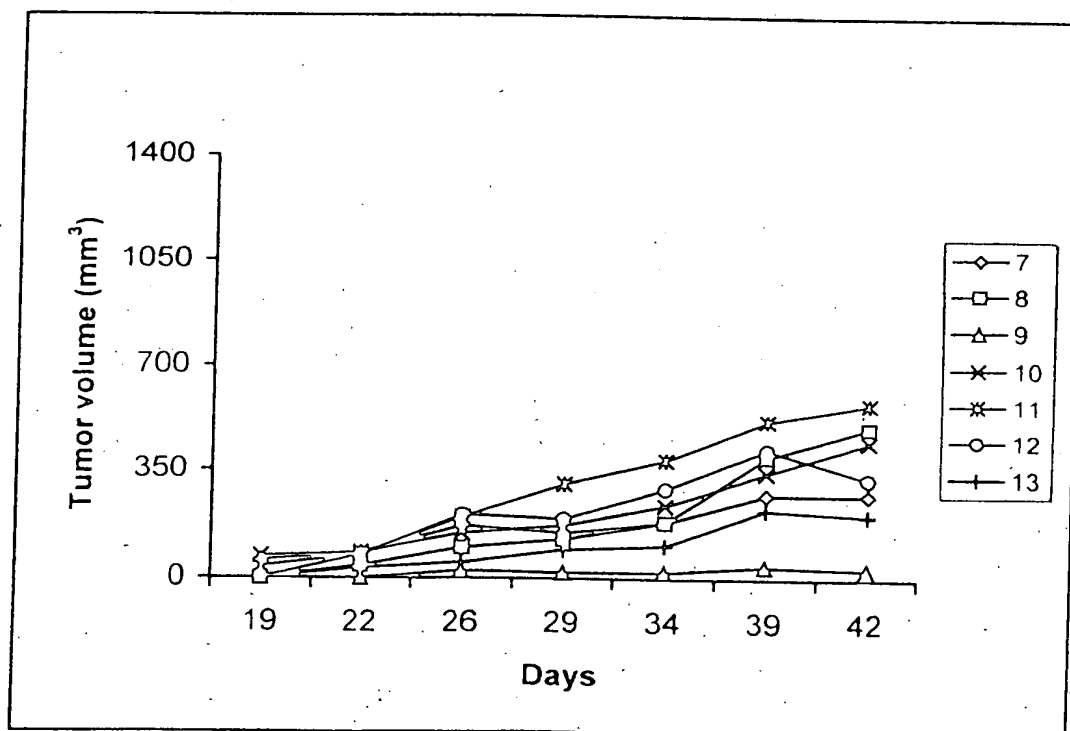
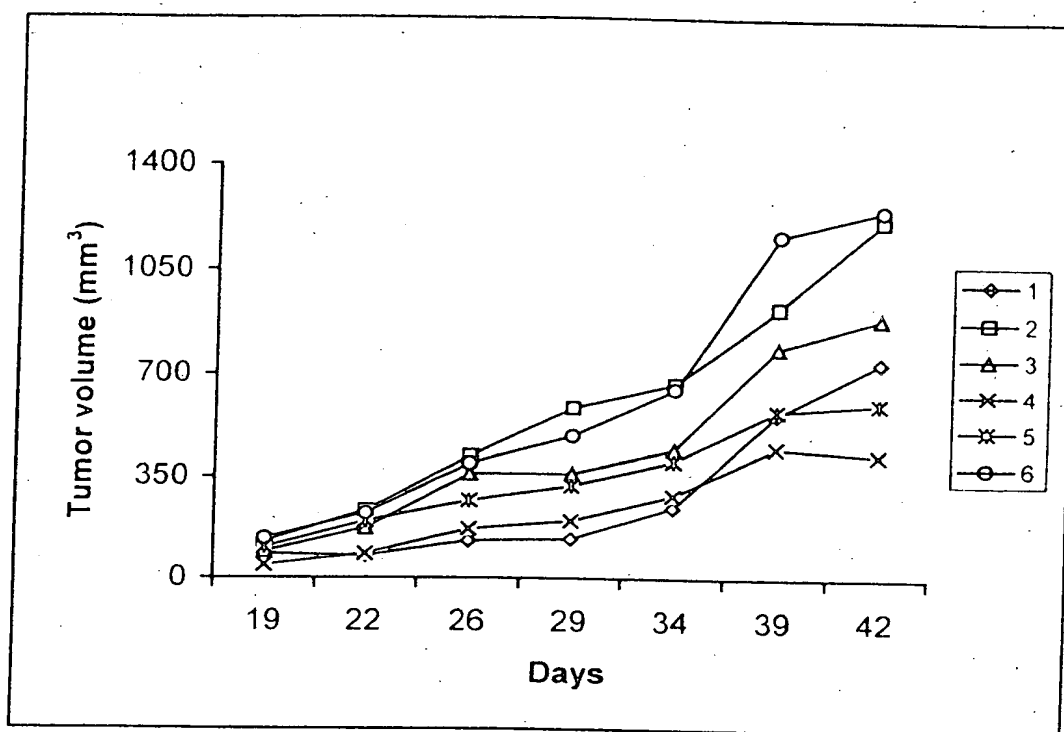
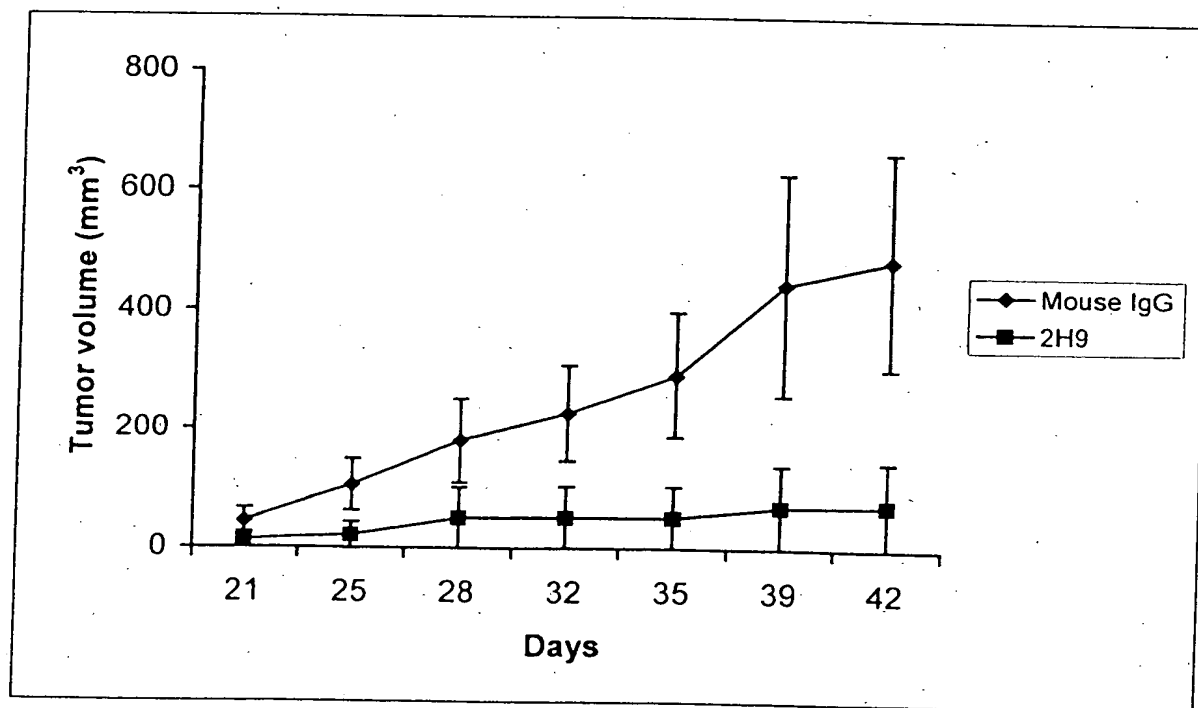
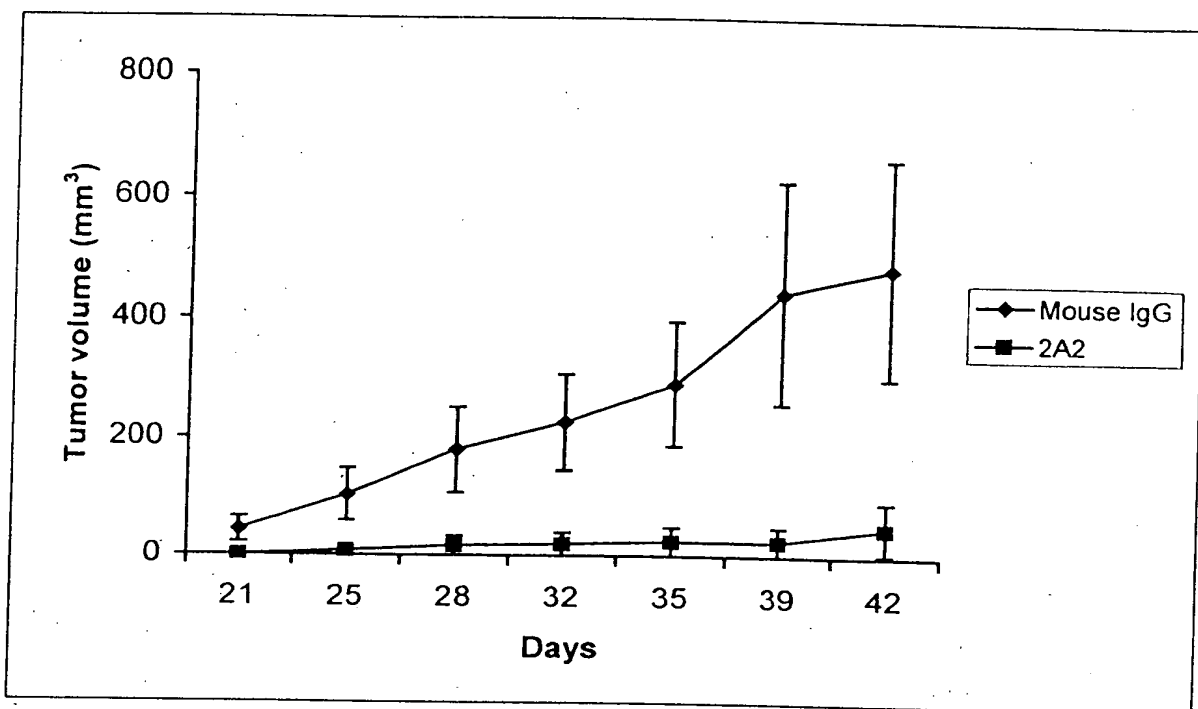


FIG. 55



TOP SECRET 6915560

FIG. 56

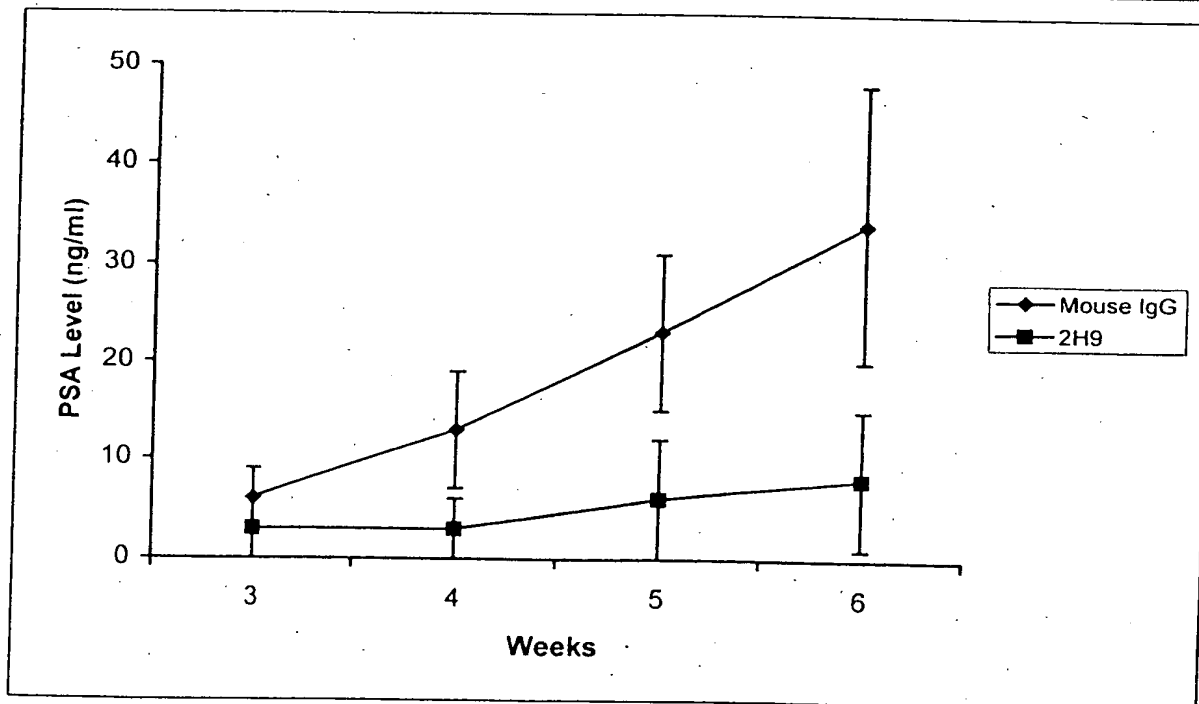
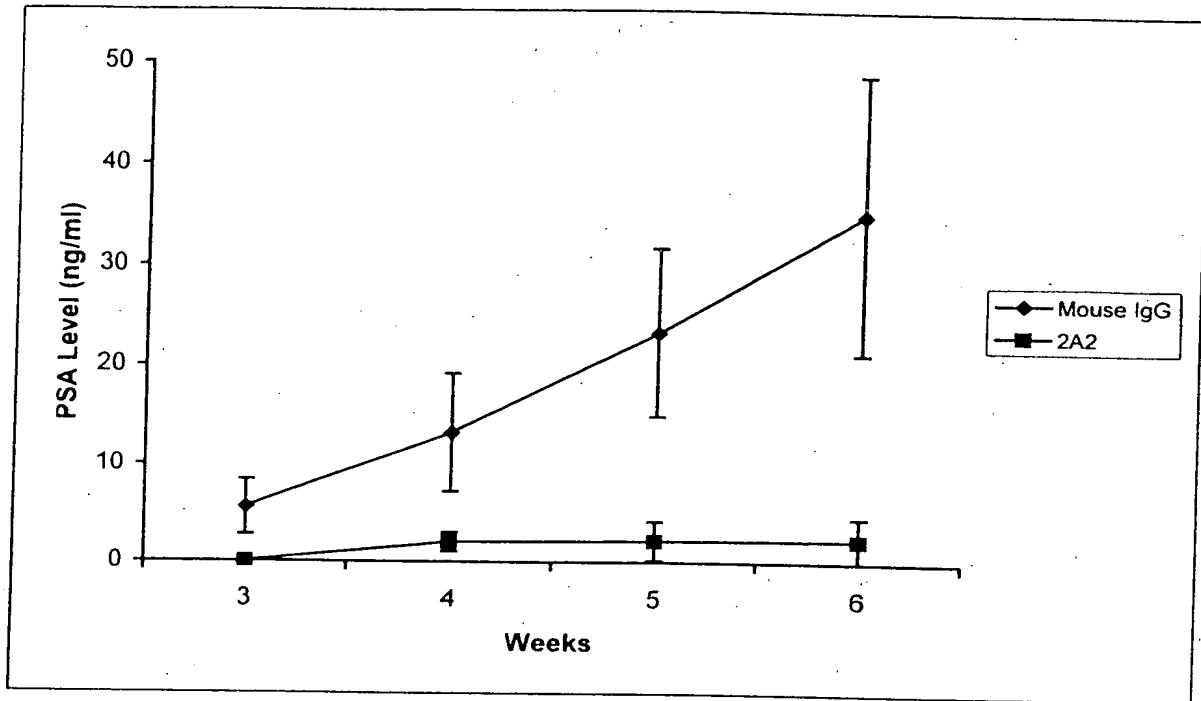


FIG. 57

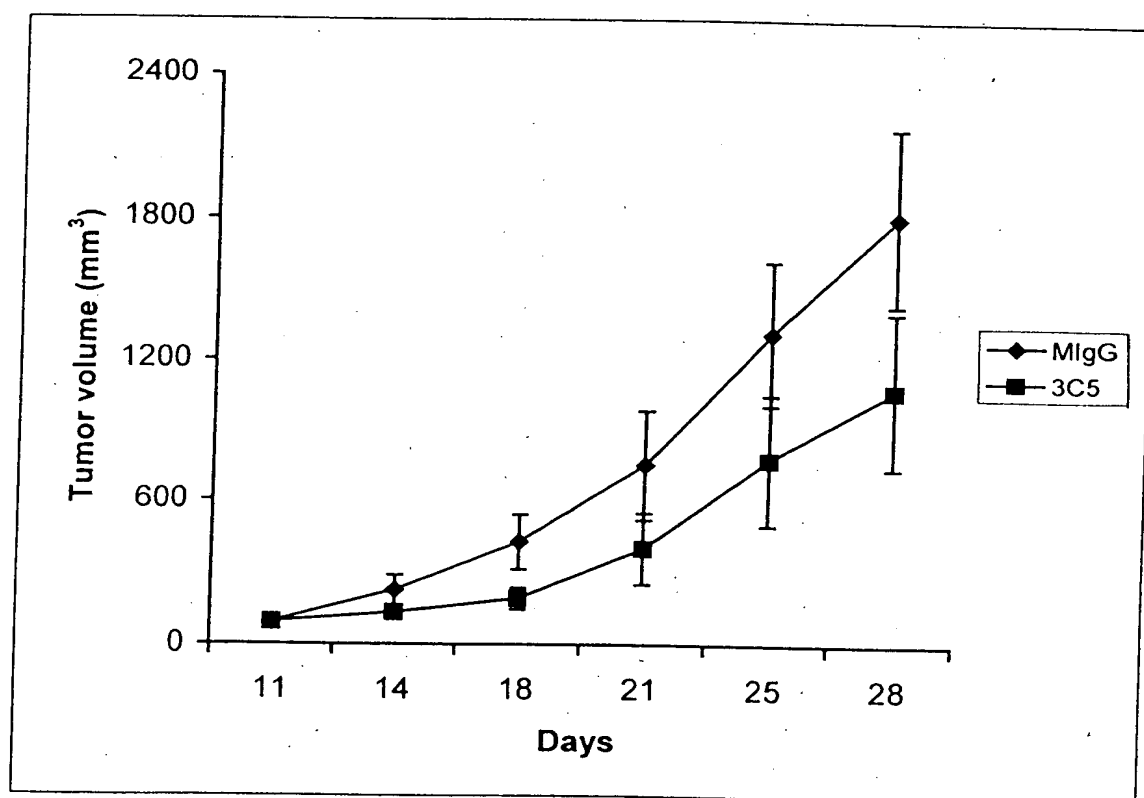


FIG. 58

TGCTTCTTCCTGATGGCAGTGGTTATAGGAGTCAATTACAGAGTTACAGCTGCAGCAGTCT 60
C F F L M A V V I G V N S E V Q L Q Q S 20

GGGCAGAACTTGTGAGGTGAGGGCCCTCAGTCAAGTTGCTCTGCACAGCTTCTGGCTTC 120
G A E L V R S G A S V K L S C T A S G F 40

----- CDR1 -----
AACATTAAAGACTACTATATACACTGGGTGAATCAGAGGCCCTGACCAGGGCCTGGAGTGG 180
N I K D Y Y I H W V N Q R P D Q G L E W 60

ATTGGATGGATTGATCCTGAGAATGGTGACACTGAATTTGTCCCGAAGTCCAGGGCAAG 240
I G W I D P E N G D T E F V P K F Q G K 80

GCCACTATGACTGCAGACATTTTCTCCAACACAGCCCTACCTGCACCTCAGCAGCCTGACA 300
A T M T A D I F S N T A Y L H L S S L T 100

TCTGAAGACACTGCCGTCTATTACTGTAAACGGGGGTTTCTGGGGCCCAAGGACTCTG 360
S E D T A V Y Y C K T G G F W G Q G T L 120

GTCACGTCTCTGCAGCCAAACGACACCCCATCTGTCTATCCACTG
V T V S A A K T T P P S V Y P L

FIG. 59

TTGGTAGCAACAGCCTCAGATGTCCACTCCAGGTCCAACTGCAGCAACCTGGGTCTGAA 60
L V A T A S D V H S Q V Q L Q Q P G S E 20

CTGGTGAGGCCCTGGAACCTTCAGTGAAGCTGTCTCCTGCAAGGCTTCTGGCTATACATTCTCC 120
L V R P G T S V K L S C K A S G Y T F S 40
CDR1

AGCTACTGGATGCACCTGGGTGAAGCAGAGGCCCTGGACAAGGCCTTGAGTGGATTGGAAT 180
S Y W M H W V K Q R P G Q G L E W I G N 60

ATTGACCCCTGGTAGTGGTTACACTAACTACGCTGAGAACCTCAAGACCAAGGCCACACTG 240
I D P G S G Y T N Y A E N L K T K A T L 80
CDR2

ACTGTAGACACATCCTCCAGCACAGCCTACATGCAGCTCAGCAGCCTGACATCTGAGGAC 300
T V D T S S S T A Y M Q L S S L T S E D 100

TCTGCAGTCTATTACTGTACAAGCCGATCTACTATGATTACGACGGGATTGCTTACTGG 360
S A V Y Y C T S R S T M I T T G F A Y W 120
CDR3

GGCCAAGGGACTCTGGTCACTGTCTCTGCAGCTACAACAACAGCCCACTGTCTATCCA 420
G Q G T L V T V S A A T T A P S V Y P 160

CTGGCC
L A

FIG. 60

AATGACTTCGGGTTGAGCTGGGTTTTATTATTATTGTTCTTTTAAAGGGGTCGGAGTGAA 60
N D F G L S W V F I I V L L K G V R S E 20

GTGAGGCTTGAGGAGTCTGGAGGAGGCTGGGTGCAACCTGGAGGATCCATGAAACTCTCC 120
V R L E E S G G G W V Q P G G S M K L S 40

TGTGTAGCCTCTGGATTTACTTTCAGTAATTACTGGATGACTTGGTCCGCCAGTCTCCA 180
C V A S G F T F S N Y W M T W V R Q S P 60
CDR1

GAGAAGGGCTTGAGTGGGTTGCTGAAATTCGATTGAGATCTGAAAATTATGCAACACAT 240
E K G L E W V A E I R L R S E N Y A T H 80
CDR2

TATCGGAGTCTGTGAAGGGAATTCACCATCTCAAGAGATGATTCAGAGTCGTCTC 300
Y A E S V K G K F T I S R D D S R S R L 100

TACCTGCAAAATGAACAACTTAAGACCTGAAGACAGTGAATTATTACTGTACAGATGGT 360
Y L Q M N N L R P E D S G I Y Y C T D G 120

CTGGACGACCTAACTGGGGCCAAGGACTCTGGTCACTGTCTCTGCAGCCAAAACGACA 420
L G R P N W G Q G T L V T V S A A K T T 140
CDR3

CCCCATCTGTCTATCCACTGGCCCCCTTGTA
P P S V Y P L A P C V

[illegible]

1G8	1gG _{1k}
2H9	1gG _{1k}
4A10	1gG _{2ak}

Middle	G	F	N	I	K	D	Y	Y	I	H
N-Term.	G	F	T	F	S	N	Y	W	M	T
N-Term.	G	Y	T	F	S	S	Y	W	M	H

1G8	1gG _{1k}
2H9	1gG _{1k}
4A10	1gG _{2ak}

W I D P E N G D T E F V P K F Q G
E I R L R S E N Y A T H Y A E S V K G
N I D P G S G Y T N Y A E N L K T

1G8	1gG _{1k}
2H9	1gG _{1k}
4A10	1gG _{2ak}

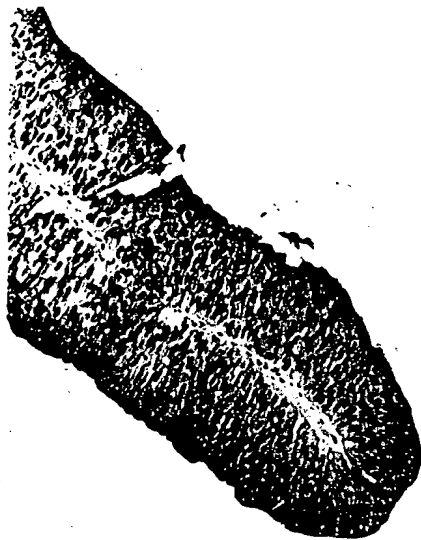
G G F
L G R P N
R S T M I T T G F A Y

FIG. 62

A



B



C



D



prostate

pancreatic

kb

9.0-

4.4-

2.4-

1.4-

1

2

3

4

5

6

7

8

9

FIG. 64

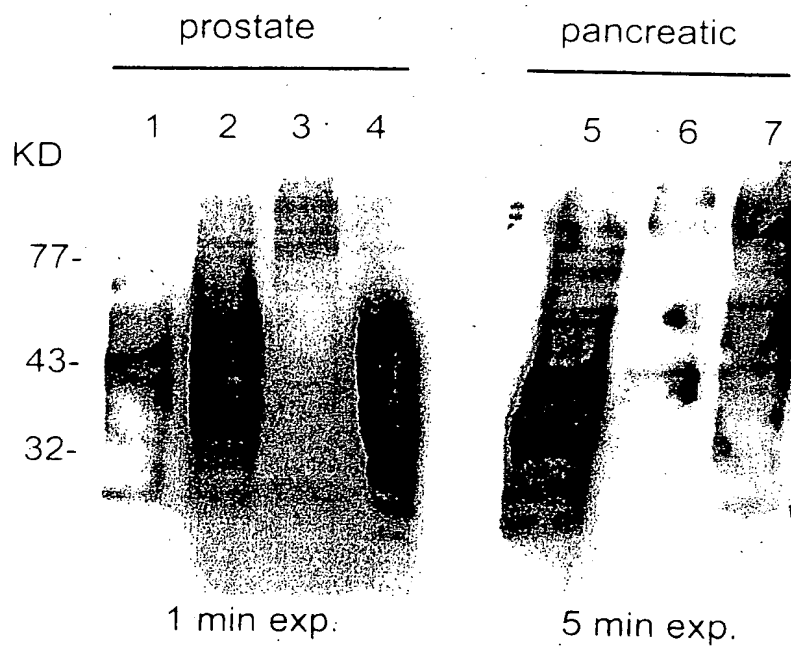


FIG. 65

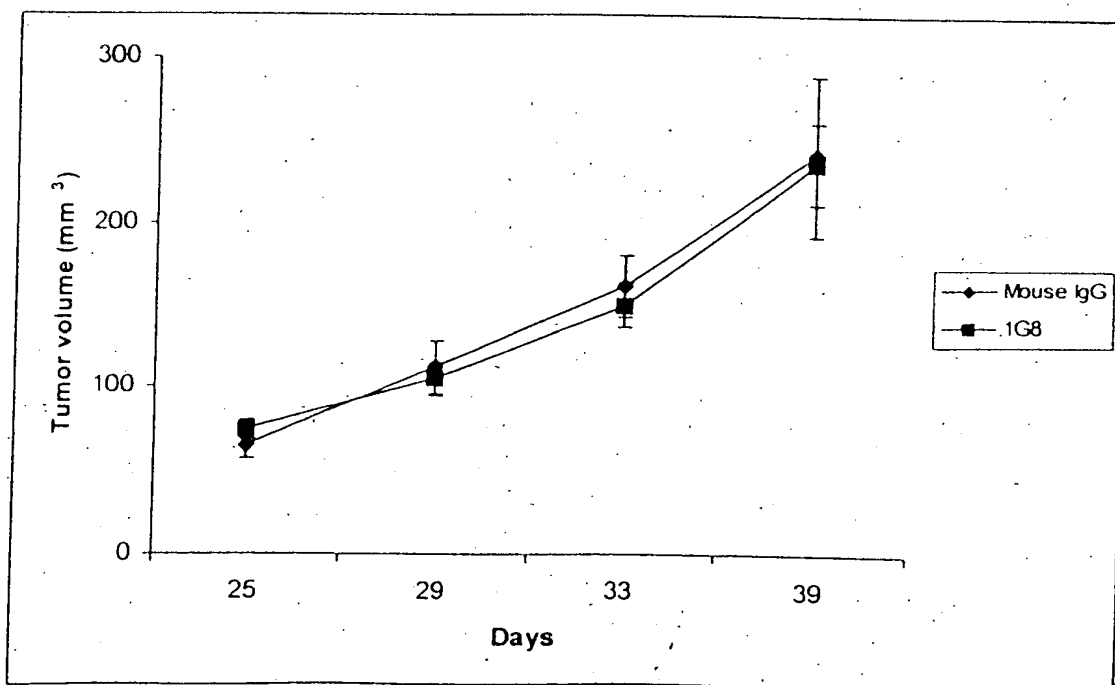
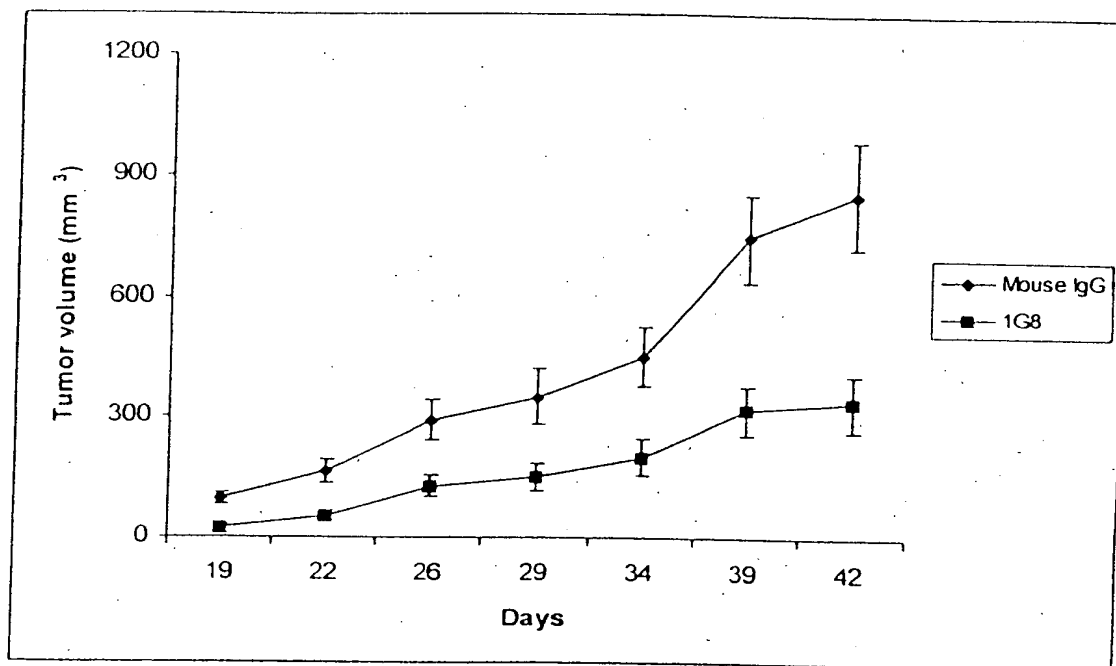
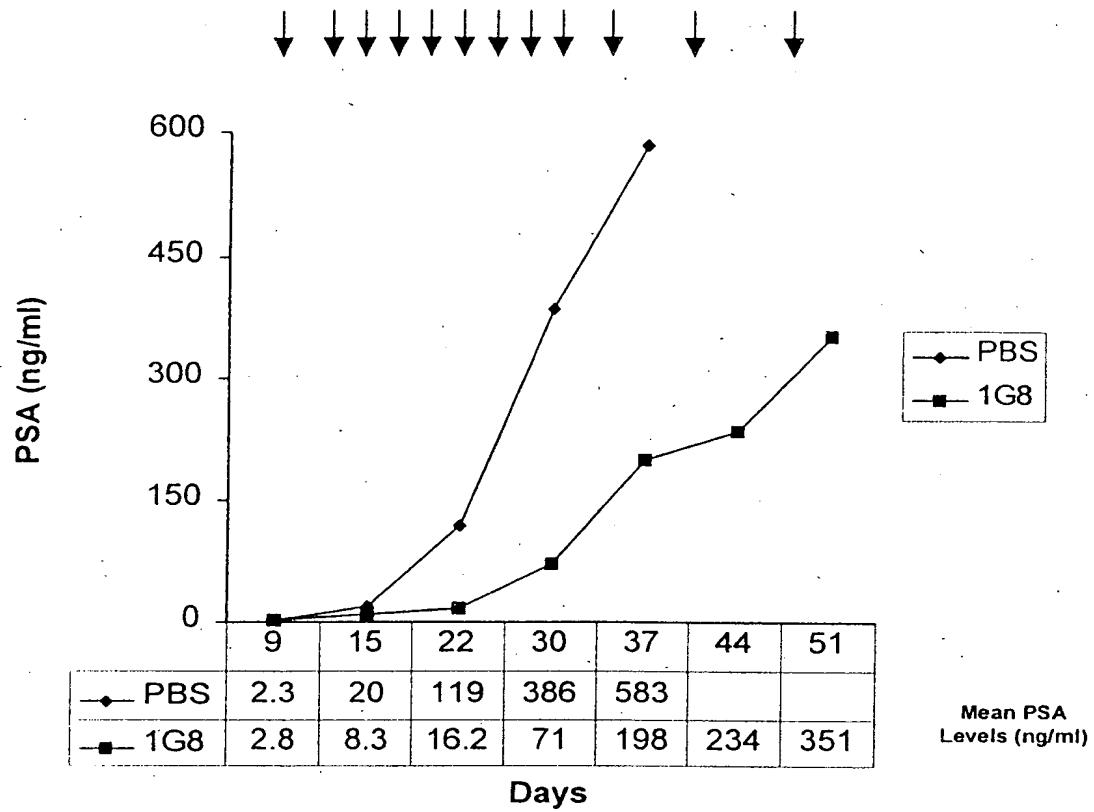


FIG. 66

A)



B)

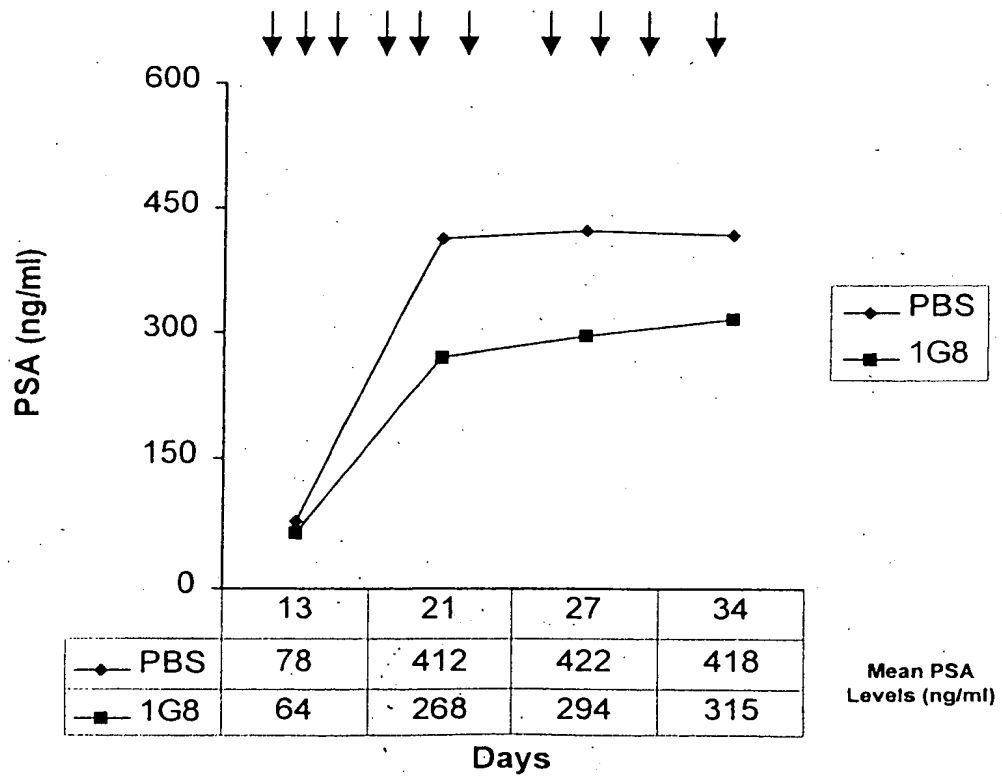
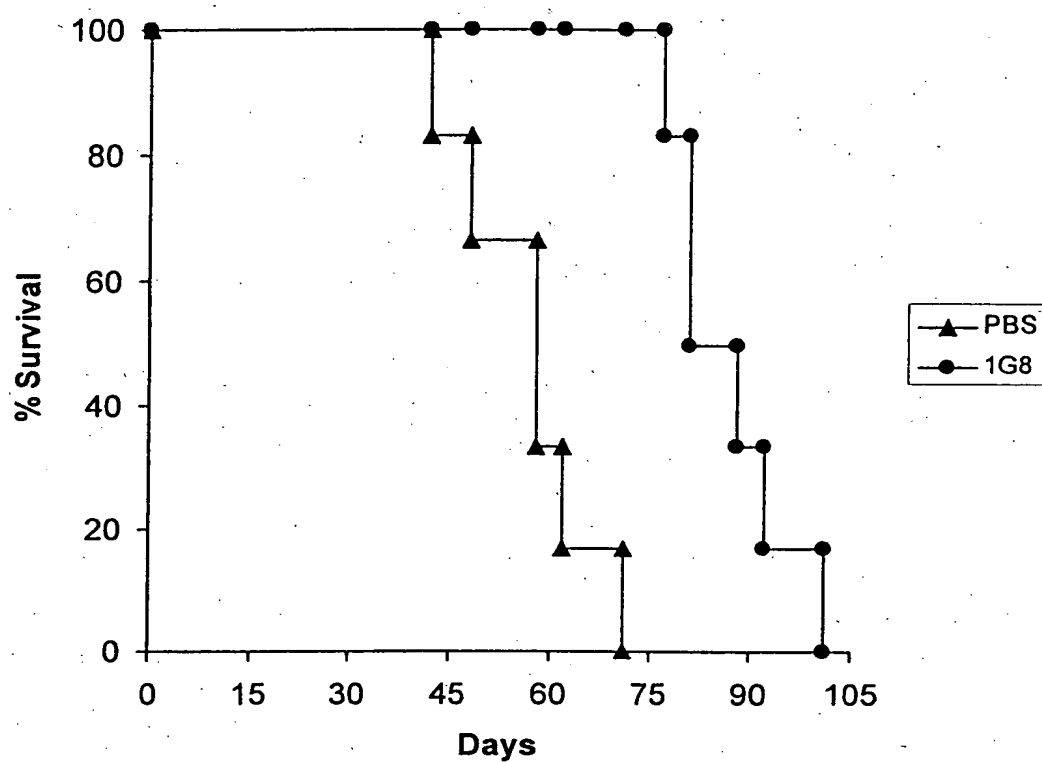


FIG. 67

A)



B)

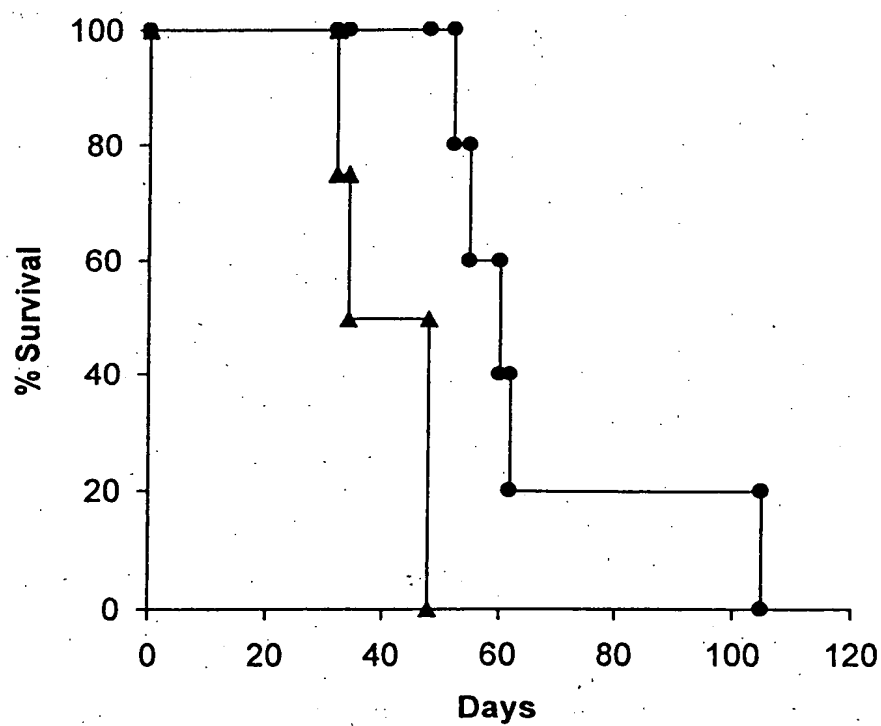
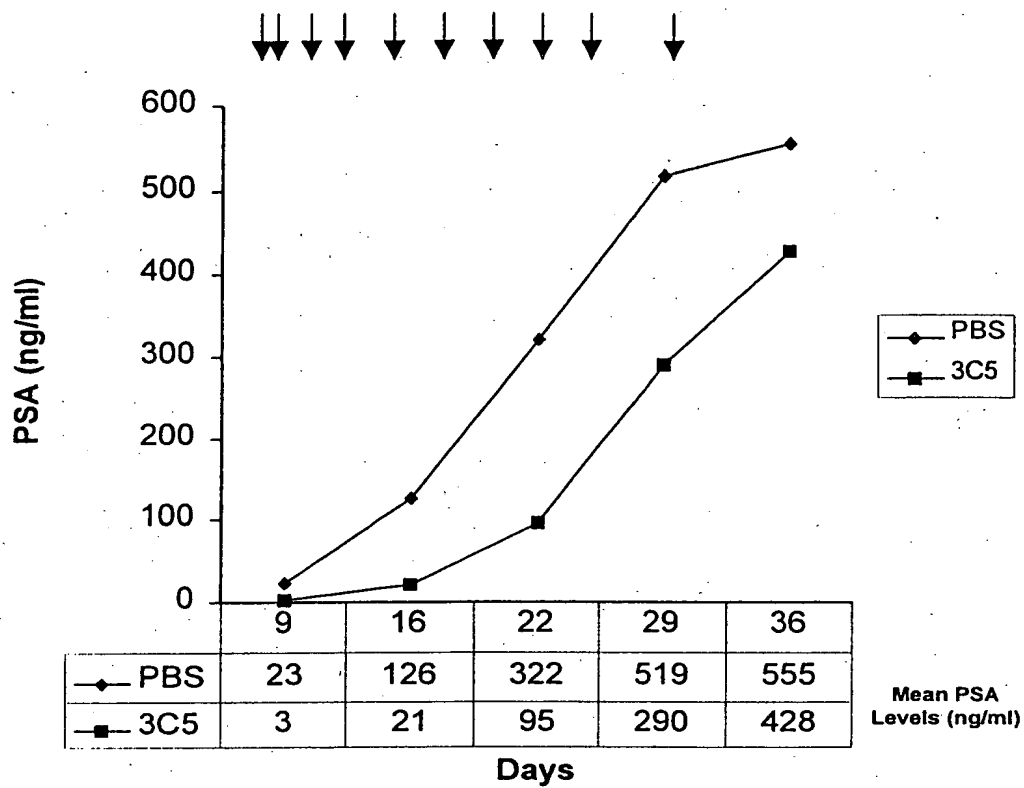


FIG. 68

A)



B)

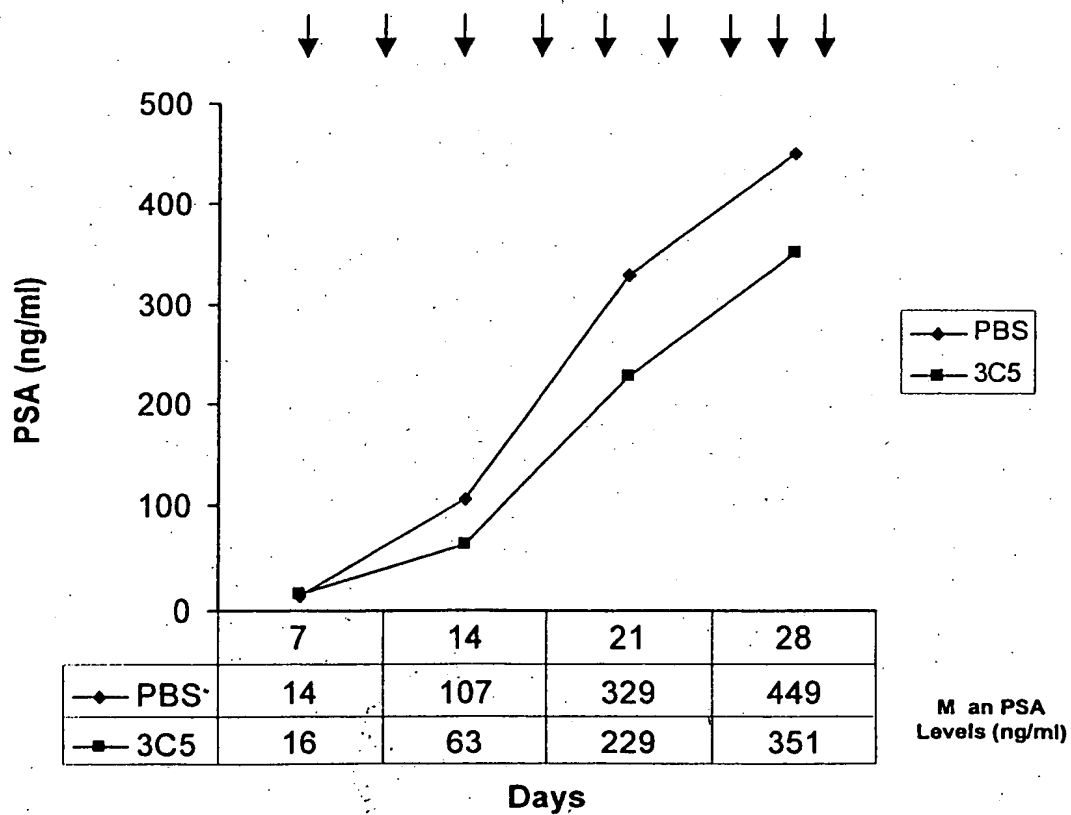
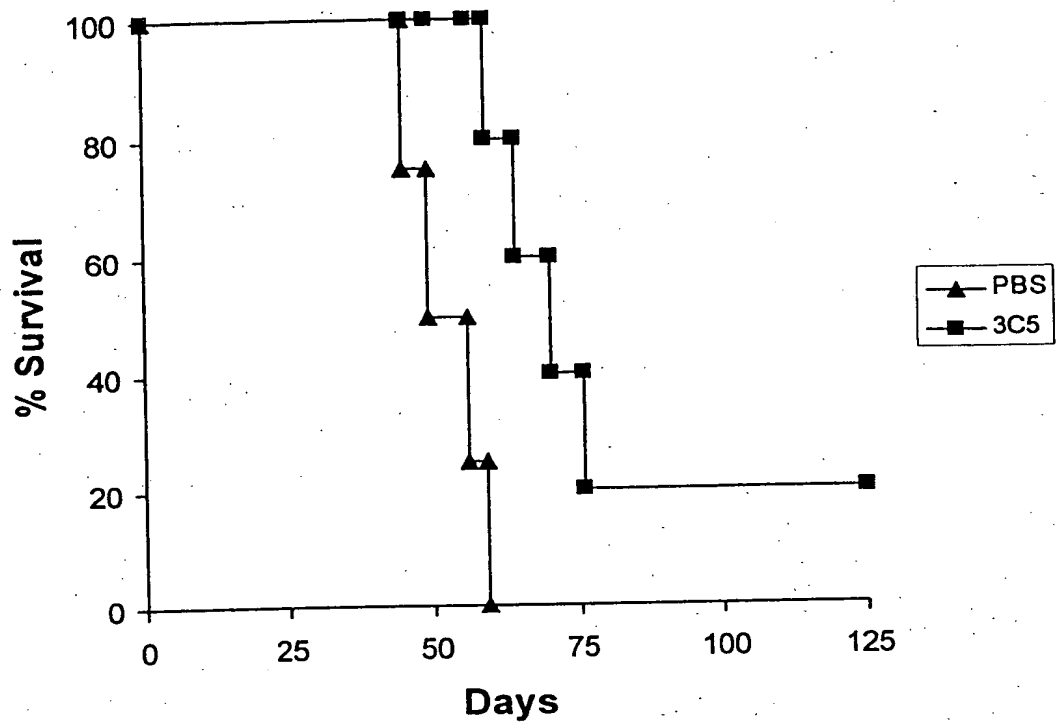


FIG. 69

A)



B)

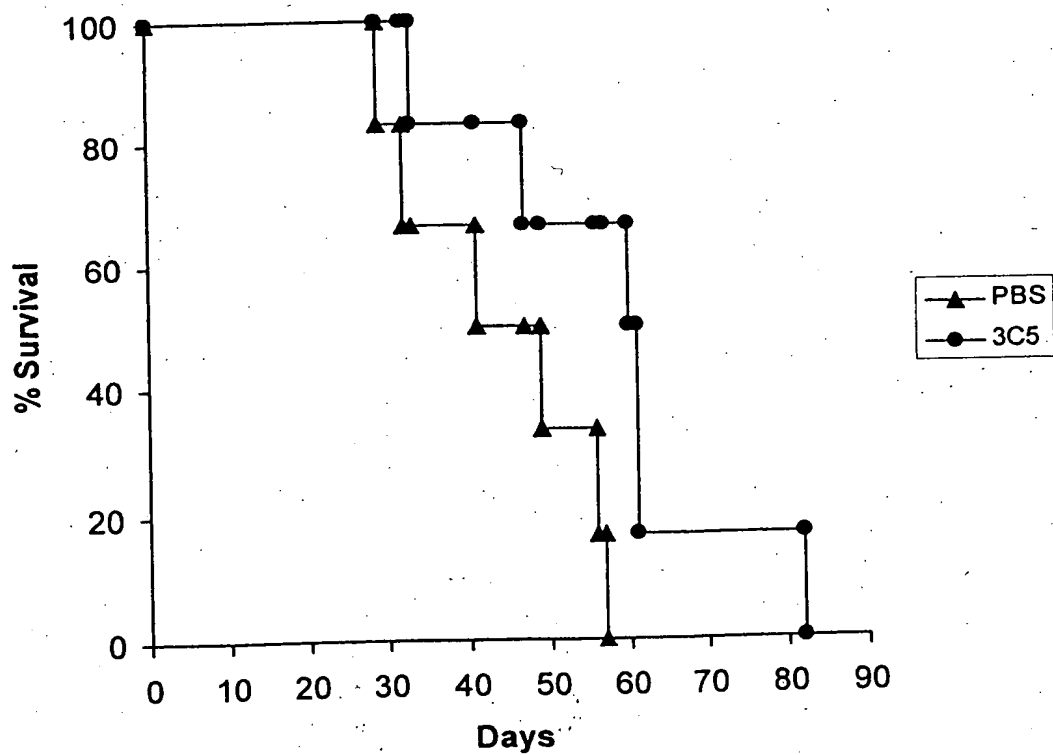
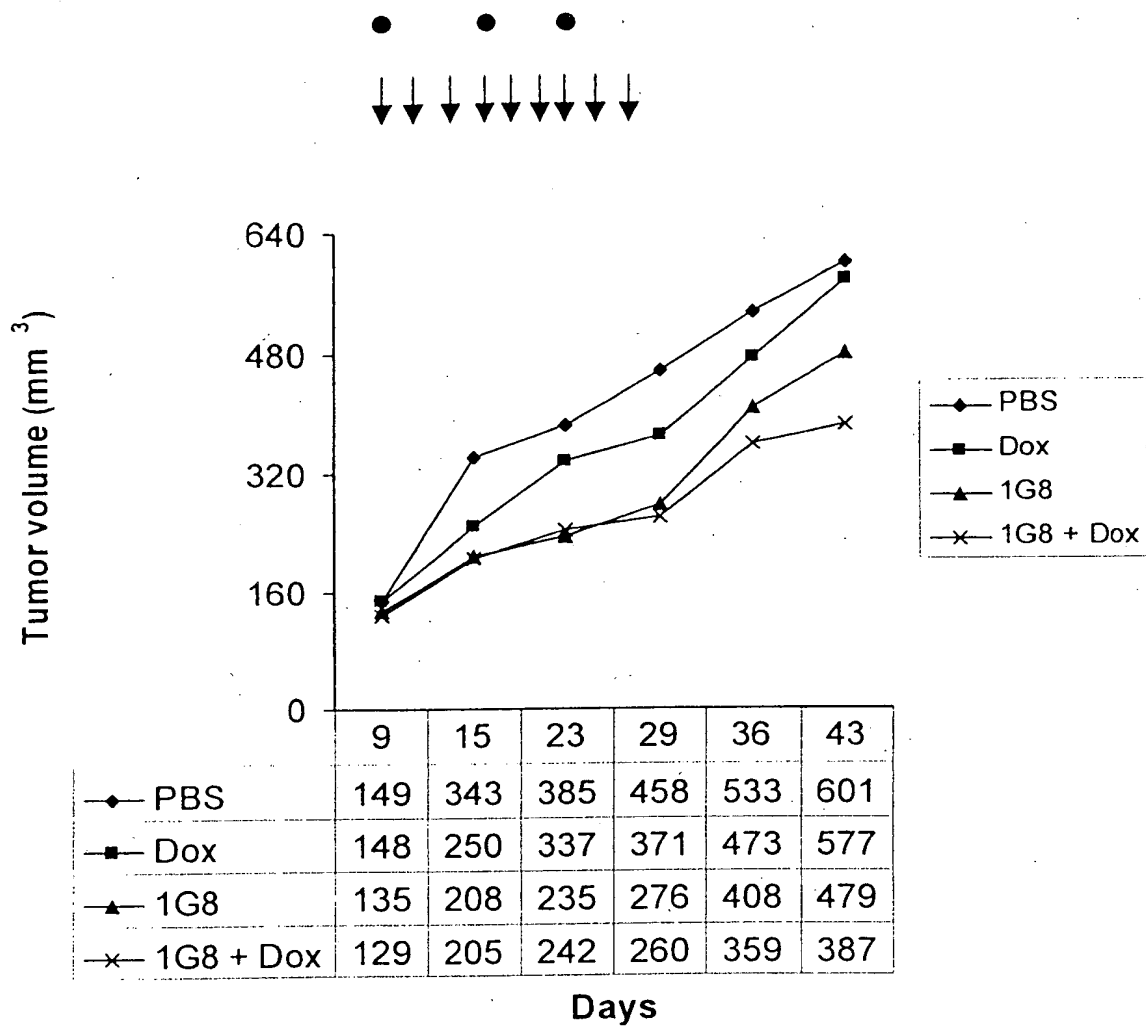


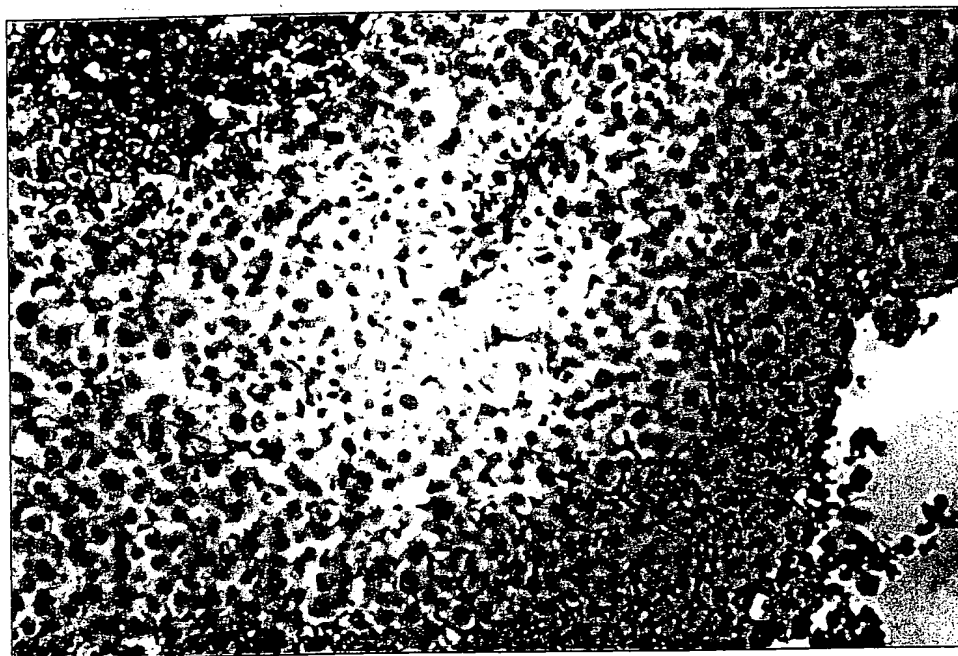
FIG. 70



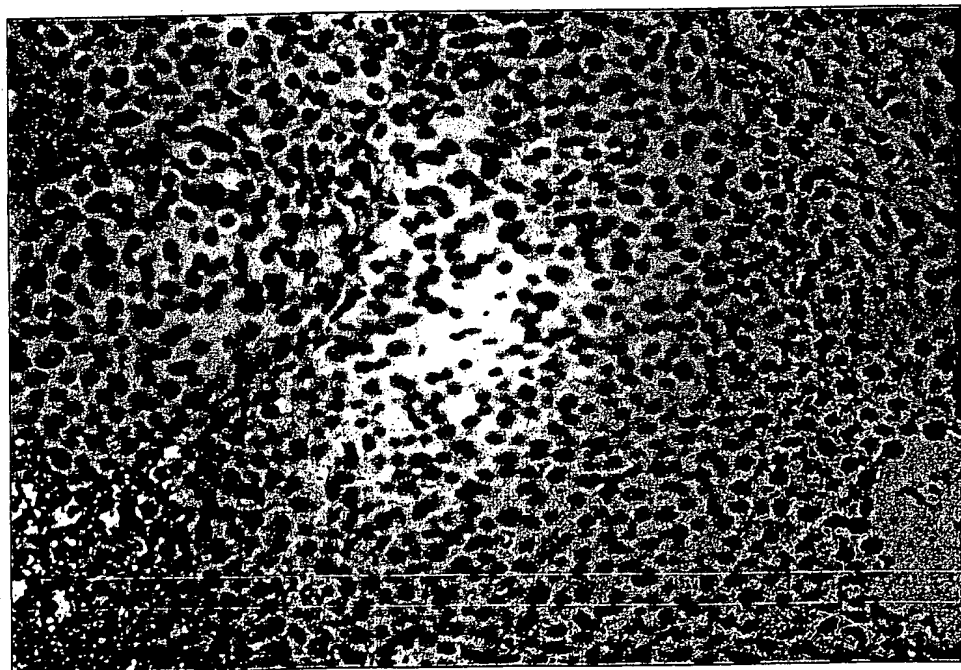
2020-04-20 14:20:00

FIG. 71

3C5 Treated



mIgG Treated



405220 6545500

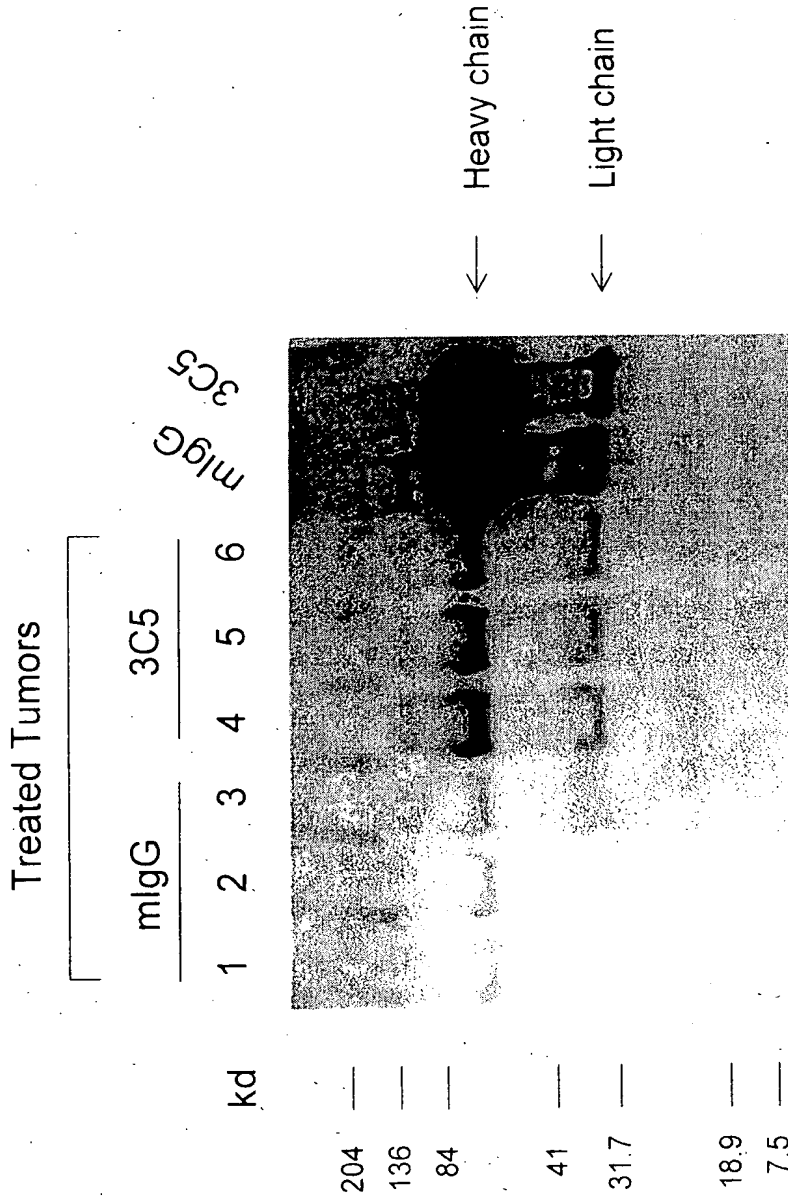


FIG. 72

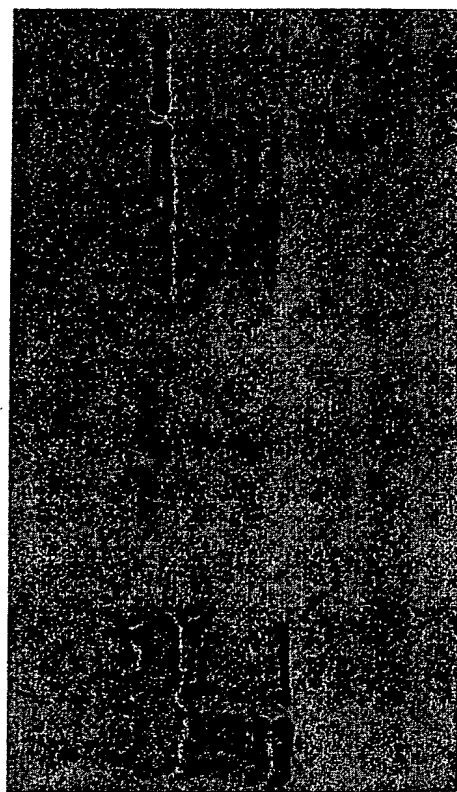
7G8
mlgG

	mlgG Treated	1G8 Treated
1	100	100
2	100	100
3	100	100
4	100	100
5	100	100
6	100	100
7	100	100
8	100	100
9	100	100
10	100	100
11	100	100
12	100	100
13	100	100
14	100	100
15	100	100
16	100	100
17	100	100
18	100	100
19	100	100
20	100	100
21	100	100
22	100	100
23	100	100
24	100	100
25	100	100
26	100	100
27	100	100
28	100	100
29	100	100
30	100	100
31	100	100
32	100	100
33	100	100
34	100	100
35	100	100
36	100	100
37	100	100
38	100	100
39	100	100
40	100	100
41	100	100
42	100	100
43	100	100
44	100	100
45	100	100
46	100	100
47	100	100
48	100	100
49	100	100
50	100	100
51	100	100
52	100	100
53	100	100
54	100	100
55	100	100
56	100	100
57	100	100
58	100	100
59	100	100
60	100	100
61	100	100
62	100	100
63	100	100
64	100	100
65	100	100
66	100	100
67	100	100
68	100	100
69	100	100
70	100	100
71	100	100
72	100	100
73	100	100
74	100	100
75	100	100
76	100	100
77	100	100
78	100	100
79	100	100
80	100	100
81	100	100
82	100	100
83	100	100
84	100	100
85	100	100
86	100	100
87	100	100
88	100	100
89	100	100
90	100	100
91	100	100
92	100	100
93	100	100
94	100	100
95	100	100
96	100	100
97	100	100
98	100	100
99	100	100
100	100	100

168

Treated

1 2 3 4 5 6



204	—
136	—
84	—
41	—
31.7	—
18.9	—
7.5	—

← Heavy chain

↓
Light chain

FIG. 73